FORM PTO-1390 (REV 10-2000) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C.371

ATTORNEY'S DOCKET NUMBER	U.S. APPLICATION NO. (If known, see 37 CFR 1.5)
PVZ-006US	09/914451

INTERNATIONAL APPLICATION	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/SE00/00384	28 February 2000 (28.02.00)	26 February 1999 (26.02.99)

TITLE OF INVENTION

DRUG DESIGN BASED ON THE STRUCTURE OF LTA_4 HYDROLASE

APPLICANT(S) FOR DO/EO/US

HAEGGSTRÖM, Jesper, Z *et al.*

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C.371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This is an express request to promptly begin national examination procedures (35 U.S.C. 371(f)).
4. ☐ The US has been elected by the expiration of 19 months from the priority date (PCT Article 31).
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
   a. ☐ is attached hereto (required only if not communicated by the International Bureau).
   b. ☒ has been communicated by the International Bureau.
   c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ An English language translation of the International Application as filed (35 U.S.C 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
   a. ☐ are attached hereto (required only if not communicated by the International Bureau).
   b. ☐ have been communicated by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☒ have not been made and will not be made.
8. ☐ An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). **(unexecuted) (4 sheets)**
10. ☐ An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included
13. ☒ A FIRST preliminary amendment. **(12 sheets) (along with version of markings to show changes)**
    ☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information: **Transmittal Letter (2 sheets in duplicate); International Application Published Under the PCT (with attached International Search Report) WO 00/50577 (156 sheets); PCT International Preliminary Examination Report (6 sheets); Certificate of Express Mailing (1 sheet); and return postcard receipt.**

JC03 Rec'd PCT/PTO 27 AUG 2001

U.S. APPLICATION NO. (if known, see 37 CFR 1.5)	INTERNATIONAL APPLICATION NO.	ATTORNEY'S DOCKET NO.
09/914451	PCT/SE00/00384	PVZ-006US

17. ☒ The following fees are submitted:

BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) .(a/o November 1, 2000):

Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO.....**$1000**

International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO **$860**

International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.455(a)(2)) paid to USPTO **$710**

International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4).....**$690**

International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4).....**$100**

CALCULATIONS PTO USE ONLY	

ENTER APPROPRIATE BASIC FEE AMOUNT =				**$1,000.00**	
Surcharge of **$130.00** for furnishing the oath or declaration later than ☒ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				**$130.00**	
CLAIMS	**NUMBER FILED**	**NUMBER EXTRA**	**RATE**		
Total claims	**50**-20 =	**30**	X **$18.00**	$ **540.00**	
Independent claims	**5** -3 =	**2**	X **$80.00**	$ **160.00**	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ **270.00**	$ **270.00**	
TOTAL OF ABOVE CALCULATIONS =				**$2,100.00**	
☒ Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.				**$1,050.00**	
SUBTOTAL =				**$1,050.00**	
Processing fee of **$130.00** for furnishing the English translation later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(f)). +				$	
TOTAL NATIONAL FEE =				**$1,050.00**	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). **$40.00** per property +				$	
TOTAL FEES ENCLOSED =				**$1,050.00**	
				Amount to be: refunded	$
				charged	$

a. ☐ A check in the amount of $_____ to cover the above fees is enclosed.

b. ☒ Please charge my Deposit Account No. 12-0080 in the amount of $1,050.00 to cover the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. **12-0080**. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:
Elizabeth A. Hanley, Esq.
LAHIVE & COCKFIELD, LLP
28 State Street
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Dated: 27 August 2001

SIGNATURE

Elizabeth A. Hanley
NAME

33,505
REGISTRATION NUMBER

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

#3

PCT Rec'd 20 DEC 2001

In re the application of: Jasper Haeggström *et al.*	**Group Art Unit:** Not Yet Assigned
Serial No.: 09/914,451	**Examiner:** Not Yet Assigned
Priority Date: February 26, 1999	
PCT Filing Date: February 28, 2000 (PCT)	
U.S. Filing Date: August 27, 2001	
For: *"Drug Design Based on the Structure of LTA$_4$ Hydrolase"*	
Attorney Docket No.: PVZ-006US	

Commissioner for Patents
BOX SEQUENCE LISTING
Washington, D.C. 20231

TRANSMITTAL LETTER FOR DISKETTE CONTAINING SEQUENCE LISTING

Dear Sir:

Responsive to the Notification of Missing Requirements Under 35 U.S.C. §371 in the United States Designated/Elected Office (DO/EO/US) dated October 22, 2001, Applicants' attorney submits a diskette containing a computer readable form of the Sequence Listing for the patent application filed on August 27, 2001. The Sequence Listing complies with the requirements of 37 C.F.R. §1.821-1.825. The material on the enclosed diskette is identical in substance to the Sequence Listing appearing on substitute pages 1 and 2 submitted herewith. The computer readable form of the Sequence Listing contained on the enclosed diskette is understood to comply with the requirements of §1.824(d).

"Express Mail" mailing label number EL 892 198 215 US

Date of Deposit December 20, 2001

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Commissioner for Patents, Box PCT, Washington, DC 20231

[signature]
Signature

Larry Taylor
Please Print Name of Person Signing

Date: **December 20, 2001**

Respectfully submitted,

LAHIVE & COCKFIELD, LLP

By: [signature]
Elizabeth A. Hanley, Esq.
Registration No. 33,505
Attorney for Applicants

IN THE UNITED STATES PATENT DESIGNATED OFFICE (DO/US)
(National Phase of International App.: PCT/SE00/00384, WO 00/50577)

In re the
application of: **Jesper Z. HAEGGSTRÖM *et al.***

International Application No.: **PCT/SE00/00384**

International Filing Date: **28 February 2000**

U.S. Serial No.: **Not Yet Assigned**

Filed: **Herewith**

For: **DRUG DESIGN BASED ON THE STRUCTURE OF LTA_4 HYDROLASE**

Attorney Docket No.: **PVZ-006US**

BOX PCT
Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Dear Sir:

Preliminary to examination of the above-referenced patent application, please amend the enclosed above-titled International patent application as follows.

In the Claims

Please amend claims 6, 9, 11, 13, 14, 15, 18, 19, 25, 28, 30, and 35 as follows.

6. (Amended) A compound which is substantially complementary to a protein according to claim 1.

9. (Amended) An isolated complex, which is comprised of a protein according to claim 1 and a complementary compound according to claim 6, wherein the three-

dimensional structure of LTA_4 hydrolase is essentially as disclosed in Table 9 by the parameters defining atom 1- atom 4876, or a functionally equivalent part, derivative or conformational analogue of such a complex.

11. (Amended) Use of the parameters of a protein according to claim 1, a compound according to claim 6 in drug design, such as in molecular modeling, direct structure-based design and/or combinatorial chemistry.

13. (Amended) Use according to claim 11, wherein said drug is for the treatment and/or prevention of disorders involving acute and chronic inflammatory and/or allergic symptoms, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis, chronic obstructive pulmonary disease (COPD), and acquired immune deficiency syndrome (AIDS).

14. (Amended) Use according to claim 11, wherein said drug is for the treatment and/or prevention of proliferative disorders, such as neoplasias and/or cancer.

15. (Amended) Use according to claim 11, wherein said drug is for the treatment and/or prevention of disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax.

18. (Amended) A method according to claim 16, wherein an enzymatic inhibitor complementary to the amino acids defined in claim 3 is screened for.

19. (Amended) An analogue obtainable by the method of claim 16.

25. (Amended) A compound obtainable by the method according to claim 21.

28. (Amended) A process for the purification of a protein according to claim 1 or obtained according to claim 26, which purification includes hydroxyapatite-based chromatography and a subsequent anion exchange chromatography.

30. (Amended) A protein obtained by the method according to claim 26.

35. (Amended) A protein according to any one of claims 6, 25, 30 or 31 for use as a medicament.

Please cancel claims 36-38.

REMARKS

Applicant amends the claims to remove multiple dependencies, to provide proper antecedent basis, and to address other matters of form. The foregoing amendments introduce no new matter and are not related to issues of patentability.

Entry of the foregoing Preliminary Amendment is respectfully in order and requested.

Attached hereto as Appendix A is a marked-up version of the changes made to the claims by the current amendments. Appendix A is captioned "Version With Markings To Show Changes Made." Also attached hereto as Appendix B is a complete set of the claims that will be pending upon entry of the amendments presented herein.

If there are any questions regarding the amendments to the application, we invite the Examiner to call Applicant's representative at the telephone number below.

Respectfully submitted,

LAHIVE & COCKFIELD, LLP

Elizabeth A. Hanley
Registration No. 33,505
Attorney for Applicants

28 State Street
Boston, MA 02109
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Date: **27 August 2001**

APPENDIX A

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Claims

Please amend claims 6, 9, 11, 13, 14, 15, 18, 19, 25, 28, 30, and 35 as follows.

6. (Amended) A compound which is substantially complementary to a protein according to ~~any one of~~ claim~~s~~ 1-~~5~~.

9. (Amended) An isolated complex, which is comprised of a protein according to claim~~s~~ 1-~~5~~ and a complementary compound according to ~~any one of~~ claim~~s~~ 6-~~8~~, wherein the three-dimensional structure of LTA_4 hydrolase is essentially as disclosed in Table 9 by the parameters defining atom 1- atom 4876, or a functionally equivalent part, derivative or conformational analogue of such a complex.

11. (Amended) Use of the parameters of a protein according to ~~any one of~~ claim~~s~~ 1-~~5~~, a compound according to ~~any one of~~ claim~~s~~ 6-~~8 or a complex according to claim 9 or 10~~ in drug design, such as in molecular modeling, direct structure-based design and/or combinatorial chemistry.

13. (Amended) Use according to claim 11 ~~or 12~~, wherein said drug is for the treatment and/or prevention of disorders involving acute and chronic inflammatory and/or allergic symptoms, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis, chronic obstructive pulmonary disease (COPD), and acquired immune deficiency syndrome (AIDS).

14. (Amended) Use according to claim 11 ~~or 12~~, wherein said drug is for the treatment and/or prevention of proliferative disorders, such as neoplasias and/or cancer.

15. (Amended) Use according to claim 11 ~~or 12~~, wherein said drug is for the treatment and/or prevention of disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax.

18. (Amended) A method according to claim 16 ~~or 17~~, wherein an enzymatic inhibitor complementary to the amino acids defined in ~~any one of~~ claim~~s~~ 3~~, 4 or 5~~ is screened for.

19. (Amended) An analogue obtainable by the method ~~according to any one~~ of claim~~s~~ 16~~-18~~.

25. (Amended) A compound obtainable by the method according to ~~any one of~~ claim~~s~~ 21~~-24~~.

28. (Amended) A process for the purification of a protein according to~~-any one of~~ claim~~s~~ 1~~-3~~ or obtained according to claim 26~~-or 27~~, which purification includes hydroxyapatite-based chromatography and a subsequent anion exchange chromatography.

30. (Amended) A protein obtained by the method according to ~~any one of~~ claim~~s~~ ~~27-29~~ 26.

35. (Amended) A protein according to any one of claims 6~~-8~~, 25, 30 or 31 for use as a medicament.

APPENDIX B

1. An isolated protein comprising at least a subsequence of the amino acid sequence of LTA_4 hydrolase, which exhibits a three-dimensional form essentially as disclosed in Table 9 by the parameters defining atom 1 to atom 4876, said subsequence being capable of participating in the control of the enzymatic pathway, such as the leukotriene cascade, or a functionally equivalent part, derivative or conformational analogue thereof.

2. A protein according to claim 1, which comprises an enzymatically active site defined in the following table:

	Left Wall	Right Wall
1		Lys608, Asp606, Lys605, Lys354, Thr355
2	Phe356, Phe362	Gln544, Asp573, Lys572, Arg568
3	Val376	Lys565, Arg540, Leu507
4	Ser380, Ser352, Glu348	Pro569
5	Tyr378, Glu348	Arg563, Glu533, Phe536, Arg537, Tyr267
6	Tyr383, Phe314, Glu318, Glu384, Arg326	
7	Gly268, Gly269, Met270	His295, Asn341, Phe340
8	Ser288, His497	Glu325, Asn291

3. A protein according to claim 2, which is an enzyme having a metallohydrolase activity capable of participating in the regulation of enzyme activities in biochemical pathways, wherein said enzymes have structures similar to the ones defined in claim 2.

4. A protein according to claim 1, which comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; Lys565.

5. A protein according to claim 1, which comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val1292; His295; Glu296; His299; Trp315; Glu318; Val322; Phe362; Val1367; Leu369; Pro374; Asp375; Ile372; Ala377; Pro382; Tyr378; Tyr383; Arg563; Lys565.

6. A compound which is substantially complementary to a protein according to claim 1.

7. A compound according to claim 6, which is substantially complementary to an enzymatically active site of said protein and which is capable of specifically inhibiting said enzymatic activity.

8. A compound according to claim 7, which is an inhibitor of a metallohydrolase enzyme.

9. An isolated complex, which is comprised of a protein according to claim 1 and a complementary compound according to claim 6, wherein the three-dimensional structure of LTA_4 hydrolase is essentially as disclosed in Table 9 by the parameters defining atom 1- atom 4876, or a functionally equivalent part, derivative or conformational analogue of such a complex.

10. A complex according to claim 9, wherein the protein complexed with LTA_4 hydrolase is selected from the group which consists of bestatin, thiolamine or hydroxamic acid or a functionally equivalent part, derivative or conformational analogue of such a complex.

11. Use of the parameters of a protein according to claim 1, a compound according to claim 6 in drug design, such as in molecular modeling, direct structure-based design and/or combinatorial chemistry.

12. Use according to claim 11, wherein said parameters are selected from the parameters disclosed in Table 9 defining atom 1- atom 4876.

13. Use according to claim 11, wherein said drug is for the treatment and/or prevention of disorders involving acute and chronic inflammatory and/or allergic symptoms, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis, chronic obstructive pulmonary disease (COPD), and acquired immune deficiency syndrome (AIDS).

14. Use according to claim 11, wherein said drug is for the treatment and/or prevention of proliferative disorders, such as neoplasias and/or cancer.

15. Use according to claim 11, wherein said drug is for the treatment and/or prevention of disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax.

16. A method for screening LTA_4 hydrolase hydrolase analogues that mimic at least a part of 5 the three-dimensional structure of the LTA_4 hydrolase molecule as defined by the parameters shown in Table 9 for atom 1 to atom 4876, which comprises the steps of
(a) producing a multiplicity of analogue structures of LTA_4 hydrolase and
(b) selecting an analogue structure, wherein the three-dimensional configuration and spatial arrangement of one or more enzymatically active sites and/or binding sites of said LTA_4 hydrolase remain substantially preserved.

17. A method according to claim 16, wherein an analogue exhibiting an enzymatic activity, such as an epoxide hydrolase and/or aminopeptidase activity, is selected.

18. A method according to claim 16, wherein an enzymatic inhibitor complementary to the amino acids defined in claim 3 is screened for.

19. An analogue obtainable by the method of claim 16.

20. An analogue according to claim 19, which exhibits an increased catalytic activity when compared to the naturally occurring form of LTA_4 hydrolase, such as defined in Table 9 by parameters of atom 1 to atom 4876.

21. A method for screening LTA_4 hydrolase binding compounds complementary to a region of LTA_4 hydrolase, preferably an enzymatically active site thereof, which comprises the steps of

(a) producing a multiplicity of possible complementary structures and

(b) selecting a structure, wherein the three-dimensional configuration and spatial arrangement of regions involved in binding to LTA_4 hydrolase remain substantially preserved, which selection is based on the three-dimensional structure of LTA_4 hydrolase, and/or LTA_4 hydrolase complexed to an inhibitor thereof, in a form adopted thereof in nature, such as defined in Table 9.

22. A method according to claim 21, wherein a general metallohydrolase inhibitor is selected, which is capable of inhibiting an enzyme belonging to the M1 family.

23. A method according to claim 21, wherein an inhibitor of the epoxide hydrolase activity and/or aminopeptidase activity of LTA_4 hydrolase or of LTA_4 syntheses is selected.

24. A method according to claim 21, wherein a compound capable of antagonizing LTB_4 receptor binding of a cell is selected.

25. A compound obtainable by the method according to claim 21.

26. A method of engineering a protein, which method comprises the steps of

- identification of a suitable set of mutations based on the structure of LTA_4 hydrolase;
- generation of a library of genes which contains the suitable sequence variations;

- selection of clones encoding the LTA_4 hydrolase analogues with a desired activity function;

wherein said desired activity is the capability of efficiently producing an organic compound of interest.

27. A method according to claim 26, wherein the specified property is the suicidal mode of action of LTA_4 hydrolase.

28. A process for the purification of a protein according to claim 1 or obtained according to claim 26, which purification includes hydroxyapatite-based chromatography and a subsequent anion exchange chromatography.

29. A process for the crystallization of an LTA_4 hydrolase, an analogue or a derivative thereof, wherein said crystallisation is performed with the addition of an ytterbium salt as an additive, such as an ytterbium chloride.

30. A protein obtained by the method according to claim 26.

31. A protein according to claim 30, which is present in an essentially pure form.

32. An isolated nucleic acid encoding a protein according to claim 30 or 31.

33. A nucleic acid capable of specifically hybridising to a nucleic acid according to claim 32.

34. Use of a protein, which is a genetically modified LTA_4 hydrolase, according to claim 30 or 31 in the preparation of LTB_4 or other metabolites in the leukotriene cascade.

35. A protein according to any one of claims 6, 25, 30 or 31 for use as a medicament.

DRUG DESIGN BASED ON THE STRUCTURE OF LTA_4 HYDROLASE

1. BACKGROUND

1.1 Technical field

The present invention relates to methods of design or identification of biologically active compounds, which methods are based on the first definition ever of a three-dimensional structure of a protein involved in the leukotriene cascade. Further, the invention relates to novel compounds obtained by said methods, to advantageous uses of such compounds as well as to processes for the preparation thereof.

1.2 Prior art

Leukotriene A4 (LTA_4) hydrolase is a pivotal enzyme in the biosynthesis of leukotrienes, a family of paracrine hormones implicated in the pathophysiology of inflammatory and allergic disorders, in particular bronchial asthma (Samuelsson, B. *Science* **220**, 568-75 (1983); and Lewis, R.A., Austen, K.F. & Soberman, R.J. *N Engl J Med* **323**, 645-55 (1990)). Leukotrienes are formed by immunocompetent cells including neutrophils, eosinophils, basophils, mast cells, and macrophages, in response to a variety of immunological as well as non-immunological stimuli. These lipid mediators are divided into two major classes exemplified by the chemotaxin LTB4, and the spasmogenic cysteinyl-leukotrienes (LTC4, LTD4, and LTE4). Leukotriene biosynthesis is initiated by the enzyme 5-lipoxygenase which converts arachidonic acid into the unstable epoxide LTA4, a central intermediate in the leukotriene cascade. LTA4 may in turn be hydrolyzed into LTB4 by the enzyme LTA4 hydrolase, or conjugated with GSH to form LTC4, a reaction catalyzed by a specific LTC4 synthase. During cellular activation, all key enzymes in leukotriene biosynthesis, except LTA4 hydrolase, form a biosynthetic complex assembled at the nuclear membrane, suggesting that leukotrienes may have unknown intranuclear functions related to gene regulation or cell growth (Serhan, C.N., Haeggstrom, J.Z. & Leslie, C.C. *Faseb J* **10**, 1147-58 (1996)).

Leukotriene B4, the natural product of LTA4 hydrolase, is one of the most powerful chemotactic agents known to date and triggers leukocyte adherence and ag-

gregation at only nM concentrations (Ford-Hutchinson, A.W., Bray, M.A., Doig, M.V., Shipley, M.E. & Smith, M.J.H. *Nature* **286**, 264-265 (1980)). Hence, this molecule is regarded as a key mediator of inflammation, and has been implicated in a number of diseases, including arthritis, psoriasis, inflammatory bowel disease (IBD), and chronic obstructive pulmonary disease (COPD). Furthermore, the role of LTB4 in inflammation has been well corroborated by the anti-inflammatory properties of LTA4 hydrolase inhibitors, particularly in combination with a cyclooxygenase inhibitor, and specific LTB4 receptor antagonists, as well as the reduced inflammatory reactions observed in several animal models of leukotriene deficiency (Tsuji, F., Miyake, Y., Enomoto, H., Horiuchi, M., Mita, S. *Eur. J. Pharmacol.* **346**, 81-85, (1998); Chen, X.S., Sheller, J.R., Johnson, E.N. & Funk, C.D. *Nature* **372**, 179-182 (1994); Griffiths, R.J., *et al. Proc Natl Acad Sci U S A* **92**, 517-21 (1995); and Griffiths, R.J., *et al. J Exp Med* **185**, 1123-9 (1997)). In addition, LTB4 modulates the immune response, *e.g.*, by interference with specific subsets of lymphocytes, production of cytokines, as well as liberation of immunoglobulins from B-lymphocytes (Payan, D.G., Missirian-Bastian, A. & Goetzl, E.J. *Proc Natl Acad Sci U S A* **81**, 3501-5 (1984); Rola-Pleszczynski, M. & Lemaire, I. *J Immunol* **135**, 3958-61 (1985); and Yamaoka, K.A., Claesson, H.E. & Rosen, A. *J Immunol* **143**, 1996-2000 (1989)). Recent data also indicate that LTB4 stimulates, and thus has a crucial role in the regulation of, cell proliferation and cell survival in HL-60 cells, suggesting that LTA4 hydrolase inhibitors may have an anti-proliferative effect. (Dittman, K.H., Mayer, C., Rodemann, H.P., Petrides, P.E., and Denzlinger, C. *Leuk. Res.* **22**, 49-53 (1998)). The cell surface receptor for LTB4 (BLTR) was recently cloned and found to be abundantly expressed in the immune system, including lymphocytes, spleen and thymus (Yokomizo, T., Izumi, T., Chang, K., Takuwa, Y. & Shimuzu, T. *Nature* **387**, 620-624 (1997)). BLTR belongs to a family of chemokine receptors and, interestingly, together with CD4 it was found to be an efficient coreceptor for HIV-1 infection (Owman, C., *et al. Proc Natl Acad Sci U S A* **95**, 9530-4 (1998)). Moreover, LTB4 is also a natural ligand to the nuclear orphan receptor PPARα,

suggesting that LTB4 may have intranuclear functions possibly related to lipid homeostasis (Devchand, P.R., *et al. Nature* **384**, 39-43 (1996)).

LTA4 hydrolase is a cytosolic 69 kDa enzyme without any similarity to other soluble or membrane bound xenobiotic epoxide hydrolases (Funk, C.D., *et al. Proc Natl Acad Sci U S A* **84**, 6677-81 (1987)). The enzyme's epoxide hydrolase activity, which generates LTB4, is highly substrate selective accepting only LTA4 and to a small extent the double bond isomers LTA3 and LTA5. Typically, LTA4 hydrolase undergoes suicide inactivation and covalent modification when exposed to LTA4 (Evans, J.F., Nathaniel, D.J., Zamboni, R.J. & Ford-Hutchinson, A.W. *J. Biol. Chem.* **260**, 10966-10970 (1985)). During this process, LTA4 apparently binds to Tyr-378, a residue which also seems to play a role for the formation of the critical *cis-trans-trans* geometry in the conjugated triene structure of LTB4 (Mueller, M.J., *et al. Proc Natl Acad Sci U S A* **93**, 5931-5935 (1996); and Mueller, M., Andberg, M., Samuelsson, B. & Haeggstrom, J. Z. *J. Biol. Chem.* **271**, 24345-24348 (1996)).

From sequence comparisons with certain metalloproteases and aminopeptidases, a zinc binding motif (HEXXH-X18-E) was unexpectedly found in LTA4 hydrolase (Vallee, B.L. & Auld, D.S. *Proc. Natl. Acad. Sci. USA* **87**, 220-224 (1990)). Further studies demonstrated that the enzyme indeed contains one catalytic zinc atom complexed to His295, His299, and Glu318 (Medina, J.F., *et al. Proc. Natl. Acad. Sci. USA* **88**, 7620-7624 (1991)). In addition, a previously unknown peptide cleaving activity was discovered which requires the presence of anions, particularly chloride (Haeggström, J.Z., Wetterholm, A., Medina, J.F. & Samuelsson, B. *J Lipid Mediator* **6**, 1-13 (1993)). Although the endogenous physiological peptidase substrate(s) has not yet been identified, LTA4 hydrolase cleaves certain arginyl di- and tripeptides with very high efficiency (Örning, L., Gierse, J.K. & Fitzpatrick, F.A. *J. Biol. Chem.* **269**, 11269-11273 (1994)). Hence, LTA4 hydrolase can be described as a bifunctional zinc metalloenzyme with the unique ability to accept both lipid and peptide substrates. Using site-directed mutagenesis, Glu296 and Tyr383 were found to be critical for the peptidase reaction, presumably as a general base and proton donor, respectively (Blomster, M., Wetterholm, A., Mueller, M.J. & Haeggström

J.Z. *Eur. J. Biochem.* **231**, 528-534 (1995); and Wetterholm, A., *et al. Proc Natl Acad Sci U SA* **89**, 9141-9145 (1992)). Since the enzyme's ability to convert LTA4 into LTB4 was not affected by the mutations, the two enzyme activities of LTA4 hydrolase are exerted via non-identical but overlapping active sites. Notably, unlike other enzymes in the leukotriene cascade, LTA4 hydrolase is ubiquitous in mammalian cells and tissues suggesting that it may have other functions presumably related to its peptide cleaving activity.

As a consequence of the identification of LTA_4 hydrolase as a zinc metalloenzyme with a peptidase activity, it was observed that LTA4 hydrolase is inhibited by bestatin, a general aminopeptidase inhibitor, and captopril, an inhibitor of angiotensin converting enzyme (Örning, L., *et al. J. Biol. Chem.* **266**, 16507-16511 (1991)).

Tsuge et al., (*J. Mol. Biol.* **238**,854-856 (1994)), have described the crystallization of LTA_4 hydrolase. However, despite the well recognized need thereof, the three-dimensional structure of LTA_4 hydrolase has not yet been disclosed. More specifically, the problems that need to be overcome in order to provide such a determination may in brief be explained as follows. There are two major difficulties in obtaining a three-dimensional structure of a protein molecule. The first one is to grow crystals of good quality that are reproducible and diffract to atomic resolution (beyond 2.5Å). This means a thorough and cumbersome investigation of parameters that influence the crystal growth such as pH, temperature, nature of buffers, nature of precipitant, just to mention a few. The addition of ligands such as substrate analogues or inhibitors or the addition of other molecules can be important for obtaining good crystals. There is only little understanding of the physical background of the crystallisation process which means that the search for suitable crystallisation conditions for a certain protein is unique, requires creativity and intuition, and is governed by trial and error procedures. The purity of the protein is also a crucial parameter in the crystallisation and a suitable degree of purity can be hard, or even imposible, to achieve. The second major difficulty is associated with overcoming the phase-problem which is inherent to X-ray diffraction methods. To be able to overcome this problem it is necessary to substitute the protein with suitable heavy

atom substance such as e.g. mercury , gold or platinum compounds. Crystals often cannot withstand the treatment with these compounds and the search for suitable substitutions is not straight forward and may become very exhaustive. Another option is to substitute all methionines by seleno-methionine (Se-Met) residues. This method requires production of recombinant protein in special strains of *E. coli* under non-standard conditions, followed by a new purification and recrystallisation of the Se-Met containing protein . Although Tsuge et al reported the crystallisation of LTA4 hydrolase, their crystals only diffracted to medium resolution and the phase-problem was not solved. Thus, as a reliable definition of the three-dimensional structure of LTA_4 hydrolase would enable e.g. a display in visual form on a computer screen of the shape of the molecule, then, could the above mentioned problems be solved, a whole range of possibilities would be opened, such as rational structure-based drug design, e.g. in combination with combinatorial chemistry, aimed at production of novel medicaments useful in disorders associated with the leukotriene cascade, as well as protein-engineering to create novel variants of the enzyme with altered, but yet useful, catalytic properties.

As LTA4 hydrolase is a recognized important drug target, some inhibitors thereof have been synthesized (Wetterholm, A., *et al. J Pharmacol Exp Ther* **275**, 31-7 (1995); and Yuan, W., Wong, C., Haeggstrom, J. Z., Wetterholm, A. & Samuelsson, B. *J. Am. Chem. Soc.*, **114**, 6552-6553 (1992)). Interestingly, certain inhibitors of LTA4 hydrolase were reported to act also as LTB4 receptor antagonists (Labaudinière R, Hilboll G, Leon-Lomeli A, Terlain B, Cavy F, Parnham M, Kuhl P, and Dereu N. *J. Med. Chem.* **35**, 3170-3179 (1992)). Due to the absence of any available information regarding the three-dimensional structure of LTA4 hydrolase, as discussed above, none of the previously described inhibitors have been designed based on the exact structure thereof. Accordingly, there is a need within this field of determining the three-dimensional structure of LTA4 hydrolase in order to design more potent and selective inhibitors of LTA4 hydrolase as well as modified structures exhibiting even more advantageous pharmaceutical properties.

2. THE PRESENT INVENTION

As the following chapter includes a substantial amount of text, it has herein been divided into separate sections, each one of which disclose separate aspects of the present invention.

Index Chapter 2

2.1 Summary of the invention

The object of the present invention is to fulfill the above defined need. This has been achieved by the crystallization and determination of the three-dimensional structure of LTA4 hydrolase complexed with the competitive inhibitor bestatin and subsequent structure determination of complexes between LTA_4 hydrolase and two specific inhibitors. It is the first three-dimensional structure of any protein component of the leukotriene cascade and enables a description of the structural basis and molecular mechanisms of various enzyme functions, such as the two catalytic activities of LTA4 hydrolase. In addition, the structural information will now make possible rational design of enzyme inhibitors, which may be developed into clinically useful anti-inflammatory drugs.

2.2 Brief description of the drawings

Figure 1 shows the key enzymes and intermediates in leukotriene biosynthesis.

Figure 2 shows 2Fo-Fc density contoured at 1.1 s. Part of the active site in the neighborhood of the bestatin molecules is shown.

Figure 3 is a ribbon diagram of the tertiary structure of leukotriene A4 hydrolase.

Figure 4 shows ribbon diagrams of the N-terminal domains of . LTA_4 hydrolase.

Figure 5 shows ribbon diagrams of the catalytic domain of LTA_4 hydrolase and thermolysin.

Figure 6 shows the structure of the C-terminal domain.

Figure 7 illustrates zinc binding ligands in LTA4 hydrolase.

Figure 8 (a) is a Ball-and-Stick presentation of the binding of bestatin in LTA4 hydrolase, while Figure 8 (b) is a schematic overview of bestatin binding in LTA4 hydrolase.

Figure 9 (a) is a wire representation of the central cavity found in LTA4 hydrolase (shown as Cα-trace).

Figure 9 (b) is a schematic presentation for the proposed binding of LTA4 into the cavity.

Figure 10 is a schematic representation for the proposed reaction mechanism of the epoxide hydrolase.

2.3 Definitions

In the present context, the term "the three-dimensional form adopted thereof in nature" is to be understood as the conformational structure, defined by the parameters x, y and z in a conventional coordinate system, that a naturally occurring molecule adapt under conditions where it is capable of exerting its biological activities.

The specific conditions during which the herein presented data were collected are detailed in the section "Experimental".

The term "isolated" and variations thereof when used in connection with a molecule, such as protein, a polypeptide or a nucleic acid, means that said molecule is isolated from other substances, such as other proteins, DNA etc normally accompanying it in its natural environment.

The term "leukotriene A_4 (LTA_4) hydrolase" as used herein is to be understood to include any mammalian or other LTA_4 hydrolase which comprises the same backbone as the human form specifically disclosed in the present application, irrespective of source. The amino acid sequences of mammalian LTA_4 hydrolase have been shown to be identical to about 90%. Thus, the three-dimensional structures thereof may be suspected to be identical to approximately the same extent.

"Thiolamine" and "hydroxamic acid" are used herein to denote the compounds examplified in the Experimental section of the present specification.

A "complementary compound" means any compound, the structure of which enables a binding thereof to a specified protein, i.e a compound having a conformation or structure enabling such a suitable fit as to provide an energetically favorable interaction between protein-complementary compound.

"Analogue" means, as used herein, a chemically altered molecule which shares the backbone with, or at least structurally resembles, a "parent molecule". In the present specification, such a "parent molecule" may be LTA_4 hydrolase or an inhibitor thereof.

In the present application, the term "active site" is to be understood to include any region capable of binding a substrate and converting it into product.

The term "nucleic acid" refers to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, encompasses known analogs of nucleotides, that can function in a similar manner as naturally occurring nucleotides.

The phrase "hybridising specifically to" refers to the binding, duplexing, or hybridising of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) of DNA or RNA. The term "stringent conditions" refers to conditions under which a probe will hybridise to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridise specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point Tm for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridise to the target sequence at equilibrium. (As the target sequences are generally present in excess, at Tm, 50% of the probes are occupies at equilibrium). Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60°C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

"Essentially pure" means herein a purity of at least about 80%, especially at least about 90% and preferably at least about 95%, such as 98-99%. The purity of

LTA_4 hydrolase, an analogue or inhibitor thereof is according to the present invention preferably determined by general biochemical and biophysical methods well-known to the skilled in this field. For proteins, SDS polyacrylamide gel electrophoresis (SDS-PAGE) with Coomassie and silver staining or amino acid sequence analysis can be used, whereas high-pressure liquid chromatography (HPLC), gas chromatography coupled to mass spectrometry (GC-MS), and nuclear magnetic resonance spectroscopy (NMR) are suitable methods for small organic molecules (peptides, lipids, or carbohydrates, or combinations of these classes of substances).

2.4 Detailed description of the invention

2.4.1 LTA_4 hydrolase, subsequences and analogues thereof

In a first aspect, the present invention relates to an isolated protein comprising at least a subsequence of the amino acid sequence of leukotriene A_4 (LTA_4) hydrolase, which subsequence has the corresponding three-dimensional form adopted thereof in nature. The protein according to invention as discussed below and elsewhere in this application is also understood to encompass any other functionally equivalent part, derivative or conformational analogue thereof. More specifically, the invention relates to the above disclosed protein which comprises a subsequence of the amino acid sequence of leukotriene A_4 (LTA_4) hydrolase, which is able to participate in, and influence, e.g. by providing enzymatic activity, the leukotriene cascade. Most preferably, the protein according to the invention is capable of controling said cascade by exerting an enzymatic activity and thus regulate the production of leukotriene B_4 (LTB_4). In a particular embodiment, the protein is comprised of essentially all of the amino acid sequence of leukotriene A_4 (LTA_4) hydrolase as disclosed in SEQ ID NO 1, or a functionally equivalent part, derivative or conformational analogue thereof.

Thus, the present invention relates to an isolated LTA_4 hydrolase in its naturally ocurring three-dimensional form. More specifically, the present application provides a listing illustrating, for the first time, the coordinates defining human LTA_4 hydrolase complexed to an inhibitor thereof. Thus, the coordinates defining the conformation of LTA_4 hydrolase have been determined by the present inventors as com-

plexed with bestatin, thiolamine and hydroxamic acid, respectively. Bestatin is a universal inhibitor of amino peptidase activity (see e.g. Mathé, G. *Biochem. Pharmacol.* 45, 49-54 (1991)), while the last mentioned two are specific inhibitors of LTA_4 hydrolase. Based on these different activities, said inhibitors may be used as models in the design of novel molecules having desired properties. Methods for such design will be discussed in further detail below as a further advantageous aspect of the invention. For reasons of conveniance for the reader of the present specification, the data collection comprising the novel coordinates according to the invention is included in the present description as a separate section denoted "X-ray data", as Table 9, immediately preceding the claims. In said table, atom no 1 to atom no 4876 define the LTA_4 hydrolase part of the complex. (protein part), atom no 4877 refers to Zn, atom nos. 4878-4880 refer to Yb, atom nos. 4881-4885 refer to imidazole, atom nos. 4886-4889 refer to acetate, atom nos 4890-4908 refer to thiolamine while atom nos. 4909-5160 refer to water. Thus, the intervening atoms relate to the metals that bind in LTA_4 hydrolase, i.e. the active site Zn atom and the Yb atoms that were crucial for the present structure determination. The conditions prevailing at the determination thereof will be described in detail in the Experimental section below. As the skilled in this field realises, such coordinates usually exhibit a certain degree of variation, due to e.g. thermal motion and slight differences in crystal packing. Thus, any references herein to Table 9 in connection with the proteins and other molecules are merely intended to illustrate an average value for each of the coordinates defining the conformation of the molecules under identical conditions, as determined by use of the same apparatus and method. Accordingly, this embodiment of the invention is not limited to a molecule having exactly the specified coordinates, but rather to molecules capable of adopting such a structure. For example, a human LTA_4 hydrolase according to the invention will exhibit a strong bit a conformational similarity with the coordinates presented by atom nos 1 - 4876 of Table 9, wherein a variation of about 1%, or 0.5 Å, may be expected. Accordingly, any such variants are within the scope of the present invention.

As regards amino acid sequence, in a specific embodiment, the protein according to the invention is identical, by direct sequence comparison, to at least about

50%, more specifically, at least about 70%, such as at least about 90%, to the LTA_4 hydrolase as defined by SEQ ID NO. 1 while in the three-dimensional form adopted thereof in nature. In this context, it is noted that the amino acid sequence of LTA_4 hydrolase also appears from the data of Table 9, but is also included as a separate sequence listing for reasons of clarity. The protein of this embodiment of the invention are e.g. variants originating from any species, preferably mammals, such as humans, mice or other rodents, etc. Alternatively, the variants including subsequences of the human sequence are mutated forms, resulting from either spontaneous mutations or deliberately produced mutations, as discussed in more detail below.

One preferred embodiment of the present invention is a protein which comprises at least one of the regions defined below in Tables 1-3 below as active sites.

Table 1: Residues lining the big cavity from outsite to insite

	Left wall	Right wall
1		Lys608, Asp606, Lys605, Lys354, Thr355
2	Phe356, Phe362	Gln544, Asp573, Lys572, Arg568
3	Val376	Lys565, Arg540, Leu507
4	Ser380, Ser352, Glu348	Pro569
5	Tyr378, Glu348	Arg563, Glu533, Phe536, Arg537, Tyr267
6	Tyr383, Phe314, Glu318, Glu384, Arg326	
7	Gly268, Gly269, Met270	His295, Asn341, Phe340
8	Ser288, His497	Glu325, Asn291

In Table 1, Lys565, Ser380, Pro569, Glu533, Tyr383, Phe314, Glu318, Glu384, Arg326, Gly268, Gly269, Met270, His295, Phe340, Ser288, and Glu325 are strictly conserved amino acids, while Lys608, Phe356, Phe362, Lys572, Arg568, Tyr378, Phe536, Tyr 267, and Asn291 are conserved in nature.

Table 2: Amino-acids in the bestatin binding site ("basic" amino-peptidase site)

The binding of bestatin to LTA_4 hydrolase may also be described by way of coordinates. Below follows the specific amino acids involved in the binding of bestatin and similar structures, as defined according to the invention.

Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; Lys565.

Table 3: Amino acids in the leukotriene binding site

The present amino acids define the site binding leukotriene-based inhibitors, such as thiolamine and hydroxamic acid, as shown in Table 9 for thiolamine.

Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Trp315; Glu318; Val322; Phe362; Val367; Leu369; Pro374; Asp375; Ile372; Ala377; Pro382; Tyr378; Tyr383; Arg563; Lys565.

In Tables 1-3 above, the enumeration of the amino acid sequence of LTA_4 hydrolase begin without the initial Met. Thus, compared to SEQ ID NO 1, which includes the initial Met, the amino acid enumeration above is lowered by one. Accordingly, Gln136 above corresponds to Gln 137 of SED ID NO 1, Ala137 above corresponds to Ala 138 of SEQ ID NO 1, etc.

Table 4: General catalytic domain for the M1 class of enzymes

Amino acids no. 210-450.

The present region will provide a basis for the development of enzyme inhibitors useful in the control other biological pathways than the leukotriene cascade.

Thus, as regards the above defined region of aminopeptidase activity of LTA_4 hydrolase, the present inventors have surprisingly observed, that said region is in fact universal for all enzymes belonging to the metallohydrolase family denoted M1.

Thus, this specific subsequence of LTA_4 hydrolase is encompassed by the present invention as a novel protein *per se*. In addition to the various advantageous uses of subsequences of LTA_4 hydrolase described herein in connection with the leukotriene cascade, this region, which is shared between all M1 enzymes, will find several further applications in connection with other enzymatic pathways. For example, the present region, herein denoted the "M1 region" in order to clarify that it is shared between the M1 enzymes, may advantageously be used to produce synthetic inhibitors, or identify natural inhibitors, of any one of the other M1 enzymes. Such M1 inhibitors will be discussed below when compounds complementary to LTA_4 hydrolase are disclosed.

The above disclosed proteins and peptides comprising subunits of LTA_4 hydrolase are advantageously used e.g. as enzymes or more preferably in methods wherein novel inhibitors of enzymatic activities are identified and/or designed.

2.4.2 Compounds complementary to LTA_4 hydrolase

In a second aspect, the present invention relates to a novel compound defined by a structure substantially complementary to the above described protein, preferably identified by use of the novel LTA_4 hydrolase conformation according to the present invention. The complementary compound is a naturally occurring or synthetic protein, peptide, lipid, carbohydrate or any other organic or inorganic compound. In relation to naturally occurring compounds, it is to be understood that the present invention relates to such compounds as isolated from their natural environment, preferably identifiable by aid of the novel coordinates defining structures according to the invention, as examplified by the complementary compounds used in the complexes shown in Table 9.

In a first embodiment, the present complementary compound is substantially complementary to an enzymatically active site of the protein and is advantageously capable of specifically inhibiting an enzymatic activity of said protein. Thus, in one embodiment, the present compound is substantially complementary to parts, or all, of the "basic" aminopeptidase binding site defined in Table 2 above. Thus, the pres-

ent compound is an inhibitor capable of specifically inhibiting an aminopeptidase activity of an enzyme, preferably of LTA_4 hydrolase. In an alternative embodiment, the present compound is substantially complementary to parts, or all, of the leukotriene binding site as defined in Table 3 above. Thus, the present compound is an inhibitor capable of specifically inhibiting an epoxide hydrolase activity of an enzyme, preferably of LTA_4 hydrolase. (The inhibition of both aminopeptidase and epoxidase hydrolase is discussed in detail below in the experimental section.) As the present two binding sites of LTA_4 hydrolase overlap in part, a further embodiment is a compound which is complementary to essential parts of both of the above discussed two binding sites, in part or partially, which thus preferably is an inhibitor of both the discussed activities.

As already mentioned above, one compound which is complementary to an enzymatically active site of LTA_4 hydrolase is a compound complementary to the M1 region thereof and thus capable of partial or total inhibition of the enzymatic activity of LTA_4 hydrolase or any other metallohydrolase belonging to the M1 family. In the present application, such inhibitors will be denoted M1 inhibitors.

As the skilled in this field will realise, the present inhibitors disclosed above need not be compound that inhibit a biological activity completely, but may be capable of exerting a partially inhibiting activity, i.e, lowering the enzymatic activity.

In another embodiment, the present complementary compound is a compound which is also capable of binding to the receptor for the product of an LTA_4 hydrolase, i.e. an LTB_4 receptor, e.g. on a cell, such as a polymorphonuclear leukocyte. Thus, such a compound may be useful as an LTB_4 antagonist whereby the biological effect of LTA_4 hydrolase activity may be regulated. Accordingly, any such LTB_4 antagonist designed and/or identified using the coordinates of LTA_4 hydrolase as presented herein are also encompassed by the present invention.

In another embodiment, the present complementary compound is a compound which, apart from being capable of binding to an active site of LTA4 hydrolase, is also capable of binding to an active site of LTC4 synthase which binds the same substrate as LTA4 hydrolase, i.e. LTA4, and turns it over into LTC4 (*cf.* Fig 1) and

is thus expected to share important structural features with the active site of LTA4 hydrolase. Such a compound may be useful as an inhibitor of LTC4 biosynthesis, whereby the production thereof may be regulated. Accordingly, any such LTC4 synthase inhibitor, designed and/or identified using the coordinates of LTA4 hydrolase, are also encompassed by the present invention.

The specific properties and advantageous uses of the present compounds as well as the design and production of novel LTA_4 hydrolase inhibitors will be described in further detail below in relation to the various methods.

2.4.3 A complex of LTA_4 hydrolase and a complementary compound

In a third aspect, the present invention relates to an isolated complex comprised of a protein as described above and a compound complementary to said protein. Said complementary compound may thus be an inhibitor of one or more of the protein's enzymatic activities, such as an aminopeptidase and/or epoxide hydrolase activity, such as bestatin, hydroxamic acid or thiolamine, or leukotriene B_4 or any analogue thereof, or LTC_4 or any analogue thereof. Examples of complementary compounds are bestatin, thiolamine or hydroxamic acid. In the present context, it is to be understood that the invention also relates to specific regions of said inhibitors, that have never been specifically disclosed for the present purpose, as well as novel inhibitors identified by aid of the present invention. In specific embodiments, the complex according to the invention is composed of LTA_4 hydrolase complexed with bestatin, thiolamine or hydroxamic acid, respectively, wherein the LTA_4 hydrolase is as defined by the coordinates presented in Table 9, or any functional fragment, derivative or analogue thereof. As bestatin is aminopeptidase based, further similar and advantageous inhibitors may be developped based on the structural information for LTA_4 hydrolase complexed with bestatin, preferably combined with the specification of the binding site of Table 2. Further, as both thiolamine is leukotriene based, the information provided in Table 9, preferably combined with the specification of binding site of Table 3, will prove to be an advantageous tool in order to gain more information about such enzymatic binding and thus the development of further

novel inhibitors, the same principles applying to hydroxamic acid, which is also leukotriene based.

Accordingly, the present invention presents for the first time the coordinates defining the three-dimensional structure of a complex of LTA_4 hydrolase and an inhibitor thereof as determined by X-ray crystallography, e.g. as illustrated in Table 9. In fact, this is the first time ever to disclose the exact parameters defining the three-dimensional structure of a protein component of the leukotriene cascade. Due to these novel reliable parameters, the complex as well as the components thereof are readily distinguished from the prior art. Together with biochemical and mutagenetic data, the novel structures will provide the basis for understanding the molecular mechanisms of the aminopeptidase and epoxide hydrolase activities, as well as the enzyme's suicide inhibition. Accordingly, the present invention will open a whole range of new possibilities as regards e.g. identification and/or design of novel biologically active molecules and methods of controlling said cascade, *in vivo* or *in vitro*. Consequently, novel advantageous drugs, such as medicaments for the treatment and/or prevention of inflammatory and/or allergic diseases, may be designed, as will be discussed in further detail below.

In the present context, it is to be understood that proteins according to the invention include the naturally ocurring three dimensional forms thereof, separated and isolated from its natural environments, as well as any such protein, wherein deletions, additions and/or substitutions of the amino acid sequence have been made, provided that the three dimensional structure is substantially maintained, as the exerted biological activity is critically dependent upon the particular three-dimensional folding of the protein. The present invention also encompasses any derivative or conformational analogue of the above disclosed proteins, which has a three-dimensional structure essentially as disclosed above, or an effective part thereof having the biological activities discussed in detail below.

2.4.4 Advantageous uses of LTA_4 hydrolase, complementary compounds and complexes thereof

A fourth aspect of the present invention is the use of a protein, a complementary compound or a complex according to to the invention in drug design, such as in molecular modeling, direct structure-based design and/or combinatorial chemistry. Such methods will be disclosed in detail below. The drugs designed using the above mentioned compounds may be suitable for the treatment and/or prevention of disorders involving acute and chronic inflammatory symtoms, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis, chronic obstructive pulmonary disease (COPD), and acquired immune deficiency syndrome (AIDS). Further, such a drug may be useed for the treatment and/or prevention of proliferative disorders, such as neoplasias and/or cancer. Alternatively, a drug may be designed which is effective for the treatment and/or prevention of an inflammatory and/or allergic disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax. However, the above mentioned diseases are exemplary and other diseases or conditions not mentioned herein may also be contemplated.

In a further aspect, the present invention relates to the use of a protein having a structure substantially as defined for the LTA_4 hydrolase of the invention, or a part, analogue or derivative thereof, for screening a compound for possible medicinal activity. In the pharmaceutical industry, new or known compounds are routinely screened for new uses employing a variety of known *in vitro* or *in vivo* screens. Often such screens involve complex natural substances and are consequently expensive to carry out, and the results may be difficult to interpret. However, the knowledge of the three-dimensional protein structure according to the invention allows a preliminary screening to be carried out on the basis of the three-dimensional structure of a region thereof, and the structural similarity of a molecule which is being screened. Such screening can conveniently be carried out using computer modelling techniques, which match the three-dimensional structure of the protein or part thereof with the structure of the molecule being screened. Potential agonist or inhibitor activity may be predicted. As a result, the production efficiency, bioavail-

ability, immunogenicity, stability etc. may be favourably changed with respect to their therapeutic application.

As regards the above disclosed M1 inhibitors, these compounds will presumably find a broader field of application than the other novel inhibitors according to the invention. Thus, the novel general M1 inhibitors are advantageously used e.g. in models to disclose in further detail other enzymatic pathways. Further, they may also be used in the above mentioned type of methods of drug design etc.

2.4.5 Screening for LTA_4 hydrolase analogues

2.4.5 (a) Method

Accordingly, in another aspect, the invention relates to a method for screening LTA_4 hydrolase analogues that mimic at least a part of the three dimensional structure of LTA_4 hydrolase, which comprises the steps of

(a) producing a multiplicity of analogue structures of the LTA_4 hydrolase

(b) selecting an analogue structure represented by a three-dimensional representation wherein the three-dimensional configuration and spatial arrangement of specific regions, preferably involved in ligand binding of said LTA_4 hydrolase, remain substantially preserved.

The coordinates used are general for LTA_4 hydrolase are essentially as illustrated in Table 9, as defined by atom nos. 1-4876.

More specifically, analogue structures of LTA4 hydrolase may be screened by their ability to catalyze a particular reaction which may be monitored by chemical physical or immunological means. Furthermore, the analogue structure may be selected from its ability to produce receptor ligands or inhibitors of secondary reactions, which may be monitored directly, as examplified above, via binding assays, enzyme assays, chemical assays, or functional bioassays.

Thus, in one embodiment, the invention relates to a method of screening, wherein one or more analogues exhibiting epoxide hydrolase activity, are screened for. Thus, such a method may be based on the data of Table 9, wherein the binding of thiolamine to LTA_4 hydrolase is shown, preferably combined with the information of Table 3 regarding the active site of LTA_4 hydrolase. In one embodiment, the

invention relates to a method of screening, wherein one or more analogues exhibiting epoxide hydrolase activity, are screened for. In an alternative embodiment, the present method is used to screen for analogues exhibiting aminopeptidase activity, which method e.g. is based data concerning the binding of bestatin to LTA_4 hydrolase is used, preferably combined with the information of Table 2 regarding the active site of LTA_4 hydrolase. Thus, the present analogues will comprise a region which is essentially analogue with the regions of LTA_4 hydrolase exhibiting aminopeptidase activity, and/or analogues exhibiting epoxide hydrolase activity are selected.

In an advantageous embodiment of the screening method according to the invention, one or more analogues comprising one or more genetic modifications, as compared to the naturally occuring form of LTA_4 hydrolase, are selected.

2.4.5 (b) Analogues obtainable by the present screening method

Further, the invention also relates to a novel analogue obtainable by the method according to the invention, such as an analogue exhibiting an increased or improved or otherwise modified catalytic activity when compared to the naturally occurring form of LTA_4 hydrolase. Preferably, said catalytic activity is an epoxide hydrolase and/or aminopeptidase activity. Further, the invention relates to an analogue obtainable by the present method and capable of acting as a metallohydrolase, preferably belonging to the M1 class of metallohydrolases.

2.4.5 (c) Mutated forms of LTA_4 hydrolase obtainable by the present screening method

In one advantageous embodiment, the present invention relates to a specified analogue which is a mutated form of LTA_4 hydrolase, which analogue comprises one or more of the mutations defined in the following Tables 5-7, wherein amino acids are given in single letter code. Thus,

Q134G/A/V/L/I/S/T/D/E/N/R/H/K/P/C/M/F/Y/W indicates that residue glutamine 134, using the LTA4 hydrolase numbering scheme, is modified to an alanine, valine, a leucine and so forth.

Table 5: Mutations in the active site

Q134G/A/V/L/I/S/T/D/E/N/R/H/K/P/C/M/F/Y/W	5(1)
Q136G/A/V/L/I/S/T/D/E/N/R/H/K/P/C/M/F/Y/W	5(2)
A137G/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(3)
Y267G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/W	5(4)
G268A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(5)
G269A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	56)
M270G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/F/Y/W	5(7)
E271G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	5(8)
V292G/A/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(9)
H295/G/A/V/L/I/S/T/D/E/N/Q/R/K/P/C/M/F/Y/W	**5(10)**
E296/G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	**5(11)**
H299G/A/V/L/I/S/T/D/E/N/Q/R/K/P/C/M/F/Y/W	**5(12)**
W311G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y	5(13)
F314G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/Y/W	5(14)
W315G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y	5(15)
E318G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	**5(16)**
V322G/A/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(17)
F362G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/Y/W	5(18)
V367G/A/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(19)
L369G/A/V/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(20)
I372G/A/V/L/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(21)
P374G/A/V/L/I/S/T/D/E/N/Q/R/H/K/C/M/F/Y/W	5(22)
D375G/A/V/L/I/S/T/E/N/Q/R/H/K/P/C/M/F/Y/W	5(23)
A377G/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/Y/W	5(24)
Y378G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/W	**5(25)**
P382G/A/V/L/I/S/T/D/E/N/Q/R/H/K/C/M/F/Y/W	5(26)
Y383G/A/V/L/I/S/T/D/E/N/Q/R/H/K/P/C/M/F/W	**5(27)**
R563G/A/V/L/I/S/T/D/E/N/Q/H/K/P/C/M/F/Y/W	5(28)

More specifically, this embodiment relates to an analogue comprising any combination of at least two mutated amino acids, or any one of the above mentioned sequences of mutations, or any separate one amino acid mutation selected from the group consisting of sequences nos 1-9, 13-15, 17-24, 26 and 28, which are all novel mutations that have never been published before the present application. As two specific embodiments of the present mutations according to the invention, E271Q and D375N are mentioned, which have shown to be especially advantageous. However, the other sequences not specified above are novel in the present context and thus such specific uses thereof are within the scope of the present invention.

Table 6: Mutations of the curved outside of the N-terminal domain

R17 G/A/V/L/I/S/T/D/N/E/Q/H/K/P/C/M/F/Y/W	6(1)
K19 G/A/V/L/I/S/T/D/N/E/Q/R/H/P/C/M/F/Y/W	6(2)
H20 G/A/V/L/I/S/T/D/N/E/Q/R/K/P/C/M/F/Y/W	6(3)
H22 G/A/V/L/I/S/T/D/N/E/Q/R/K/P/C/M/F/Y/W	6(4)
R24 G/A/V/L/I/S/T/D/N/E/Q/H/K/P/C/M/F/Y/W	6(5)
D28 G/A/V/L/I/S/T/N/E/Q/R/H/K/P/C/M/F/Y/W	6(6)
T33 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(7)
T35 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(8)
G36/A/V/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(9)
T37 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(10)
A39 G/V/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(11)
T41 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(12)
Q43 G/A/V/L/I/S/T/D/N/E/R/H/K/P/C/M/F/Y/W	6(13)
K63 G/A/V/L/I/S/T/D/N/E/Q/R/H/P/C/M/F/Y/W	6(14)
V65 G/A/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(15)
N67 G/A/V/L/I/S/T/D/E/Q/R/H/K/P/C/M/F/Y/W	6(16)
N97 G/A/V/L/I/S/T/D/E/Q/R/H/K/P/C/M/F/Y/W	6(17)
E99 G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	6(18)
V101 G/A/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(19)
E103 G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	6(20)
S105 G/A/V/L/I/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(21)
E107 G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	6(22)
K153 G/A/V/L/I/S/T/D/N/E/Q/R/H/P/C/M/F/Y/W	6(23)
T155 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(24)
T157 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(25)
E159 G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	6(26)
S161 G/A/V/L/I/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(27)
D175 G/A/V/L/I/S/T/N/E/Q/R/H/K/P/C/M/F/Y/W	6(28)
E177 G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	6(29)
T178 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(30)
D180 G/A/V/L/I/S/T/N/E/Q/R/H/K/P/C/M/F/Y/W	6(31)
R186 G/A/V/L/I/S/T/D/N/E/Q/H/K/P/C/M/F/Y/W	6(32)
I188 G/A/V/L/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(33)
K190 G/A/V/L/I/S/T/D/N/E/Q/R/H/P/C/M/F/Y/W	6(34)
I192 G/A/V/L/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	6(35)
K194 G/A/V/L/I/S/T/D/N/E/Q/R/H/P/C/M/F/Y/W	6(36)

Table 7: Mutations at the proline rich region

T359 G/A/V/L/I/S/D/N/E/Q/R/H/K/P/C/M/F/Y/W	7(1)
E358 G/A/V/L/I/S/T/D/N/Q/R/H/K/P/C/M/F/Y/W	7(2)
D443 G/A/V/L/I/S/T/N/E/Q/R/H/K/P/C/M/F/Y/W	7(3)
A446 G/V/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	7(4)
Y449 G/A/V/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/W	7(5)
S450 G/A/V/L/I/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	7(6)

P451 G/A/V/L/I/S/T/D/N/E/Q/R/H/K/C/M/F/Y/W	7(7)
G452 /A/V/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	7(8)
L453 G/A/V/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	7(9)
P454 G/A/V/L/I/S/T/D/N/E/Q/R/H/K/C/M/F/Y/W	7(10)
P455 G/A/V/L/I/S/T/D/N/E/Q/R/H/K/C/M/F/Y/W	7(11)
I456 G/A/V/L/S/T/D/N/E/Q/R/H/K/P/C/M/F/Y/W	7(12)
K457 G/A/V/L/I/S/T/D/N/E/Q/R/H/P/C/M/F/Y/W	7(13)
P458 G/A/V/L/I/S/T/D/N/E/Q/R/H/K/C/M/F/Y/W	7(14)
N459 G/A/V/L/I/S/T/D/E/Q/R/H/K/P/C/M/F/Y/W	7(15)
Y460 G/A/V/L/I/S/T/D/N/E/Q/R/H/K/P/C/M/F/W	7(16)
D461 G/A/V/L/I/S/T/N/E/Q/R/H/K/P/C/M/F/Y/W	7(17)

2.4.5 (d) Nucleic acids encoding the novel compounds

Further, the invention also relates to an isolated nucleic acid encoding a novel analogue as defined above, that is, including a combination of any at least two of said mutations or one of the novel mutations, as well as a nucleic acid capable of specifically hybridising to a such a nucleic acid. The conditions of specific hybridisation are defined above in the section "Definitions". Further, the invention also relates to any vector or carrier comprising such a nucleotide, such as plasmids, viral vectors, e.g. retrovirus, oligonucleotides etc. Thus, any cell including such a nucleic acid or vector are also within the scope of the present invention and may e.g. be a mammalian cell, such as a human cell, or any other eucaryotic cell, or a procaryotic cell, such as a bacterium. The above mentioned elements may be used in the design of model systems useful in the study of the diseases discussed elsewhere in this application, which systems may be cell cultures, animal models, such as mice, etc.

2.4.6 (a) Production and purification of genetically modified forms of LTA_4 hydrolase

Yet another aspect of the present invention is a process for the production of a novel genetically modified form of LTA_4 hydrolase identified or designed according to the present invention. Thus, the present process involves, after conventional steps of insertion a gene encoding the desired product in a host cell and expression thereof, a purification procedure, which includes a hydroxyapatite-based chromatography and a subsequent anion exchange chromatography. These last two steps have been shown to be especially advantageous, in fact, even crucial, for obtaining a

satisfying purity of the novel LTA_4 hydrolase forms according to the invention. The preceding steps are conventional as disclosed in literature and are easily performed by the skilled in this field.

Thus, in more detail, the invention relates to a method for purification of LTA4 hydrolase comprised of (i) precipitation with ammonium sulphate, followed by (ii) separations on FPLC using anion exchange, hydrophobic interaction, and chromatofocusing resins, essentially as described (Wetterholm A., Medina J.F., Rådmark O., Shapiro R., Haeggström J.Z., Vallee B.L., Samuelsson B. *Biochim. Biophys. Acta.* **1080**, 96-102 (1991)). To achieve a purity suitable for crystallography, we used (iii) chromatography on hydroxyapatite, e.g., on a TSKgel HA-1000, Tosohaas, followed by (iv) a step of anion-exchange chromatography on e.g., Mono-Q HR5/5.

Further, example 4 below describes in detail a purification of LTA_4 hydrolase according to the invention. Said example may be generalised to describe further the purification according to the invention.

2.4.6 (b) Purified LTA_4 hydrolase

Further, the invention also relates to an essentially pure form of LTA_4 hydrolase obtained by the process described above.

2.4.7 Identification of LTA_4 hydrolase binding compounds

2.4.7 (a) Method

In yet a further aspect, the present invention relates to a method for screening LTA_4 hydrolase binding compounds complementary to a region, preferably an enzymatically active site, e.g. as defined in Tables 1-3, of the LTA_4 hydrolase molecule, which comprises the steps of

(a) producing a multiplicity of possible complementary structures and

(b) selecting a structure represented by a three-dimensional representation, wherein the three-dimensional configuration and spatial arrangement of regions of LTA_4 hydrolase involved in binding remain substantially preserved, which selection is based on the three-dimensional structure of LTA_4 hydrolase and/or LTA_4 hydrolase complexed to an inhibitor thereof, e.g. as defined by the coordinates of Table 9.

More specifically, the method according to the invention will advantageously be used to select compounds capable of inhibiting epoxide hydrolase activity and/or aminopeptidase activity, LTB_4 receptor antagonists or inhibitors of LTC_4 synthases or inhibitors of any member of the M1 class of metallohydrolases. In one preferred embodiment, general enzyme inhibitors are screened for, which inhibitors are useful in the control of any one of a plurality of enzymatic pathways, wherein a metallohydrolase of the M1 type is participating. These general metallohydrolase inhibitors are herein denoted M1 inhibitors.

Structure-based design of inhibitors

In a further embodiment, the present invention relates to a method of structure-based design of LTA_4 hydrolase inhibitors. Such methods are based on the use of the present coordinates, or preferably the coordinates defining a selected region, as templates in order to synthesize advantageous inhibitors with strong and specific binding properties. More specifically, said method first uses a conventional organic synthesis, alone or combined with combinatorial chemistry, wherein the structure of the product of the synthesis is then further refined by cycles of crystallisation of enzyme and inhibitor, followed by another chemical synthesis, the product of which is again refined, etc.

Example 2 describes such a design, wherein it is noted noted that the removal of an extra carbon atom could yield a compound, which is a better inhibitor than this hydroxamic acid compound. Thus, similar conclusions will be drawn from the present method and result in inhibitors with superior properties compared to any prior art inhibitors.

2.4.7 (b) Identified binding compounds

Further, the present invention also relates to any novel compounds identifiable by the present method. Advantageous and desired properties as well as other features of such compounds, e.g. as inhibitors, is discussed above in relation to complementary compounds, analogues etc. In one preferred embodiment of the invention, such an identified compound is an inhibitor of another M1 enzyme than LTA_4 hydrolase, such as . The medicinal aspects of the present compounds will be discussed below.

Protein engineering

2.4.8 (a) Method

In a further aspect, the present invention relates to a method of engineering a protein, which method comprises the steps of

-identification of a suitable set of mutation sites based on the structure of LTA_4 hydrolase according to the invention,

-generation of a library of genes which contains the suitable sequence variations;

-selection of clones encoding a LTA_4 analogue with a desired activity;

wherein said desired activity is the capability of efficiently producing organic compounds of interest.

The present method is based on recent techniques available for generating large libraries of mutated genes (>1 billion variants) which can be attributed to a selection process of individual genes in the laboratory. Such directed evolution schemes have enormous potential for the design of new proteins, including new substrate specificity for enzymes as well as improving enzyme activities.

Directed evolution, or combinatorial engineering schemes have been successfully applied in evolving RNA molecules with improved binding and catalytic activities (Lorsch and Szostak, 1994). Also binding proteins (and peptides) with good affinities can now routinely be evolved based on a range of different protein folds (Nord et al, 1997). The present methods may be used to perform such a directed evolution of advantageous enzyme activity and specificity and may be performed by someone skilled in this field with reference to the literature, see e.g. O. Kuchner and F. H. Arnold (1997); A. Crameri, S.A. Raillard, E. Bermudez and W.P.C. Stemmer (1998).) In this context, see also the descriptions provided in US patent no 5 873 082, Noguchi, wherein a list processing system for managing and processing lists of data is disclosed; US patent no 5 869 295, LaBean et al., disclosing methods and materials for producing gene libraries; and US patent no 5 856 928, disclosing a process for gene and protein representation, characterization and interpretation thereof.

In general, major difficulties in this kind of process are to search the sequence space: find the suitable sequence variations for a large but limited number of muta-

tions (for the same protein fold an immense number of variations can be made e.g. 10 resides protein, 20^{100} variants are in theory possible). It is therefor very important to identify the residues in the protein structure which could effect the activity the most, i.e. the residues near the active site area. Thus, in order to enable a successful performance of a method for engineering proteins with properties relevant in the present field, the data discosed above, more specifically, in Tables 2-4, is crucial.

Further references which are relevent in the context of protein engineering are K. Nord, E. Gunneriusson, J. Ringdahl, S. Stahl, M. Uhlen, P.A. Nygren (1997): "Binding proteins selected from combinatorial libraries of an alpha-helical bacterial receptor domain", *Nature Biotechnology* ,**15**, 772-777 (1997); R. Lorsch and J.W. Szostak (1994): "*In vitro* evolution of new ribozymes with polynucleotide kinase activity", *Nature*, **371**, 31-36; A. Crameri, S.A. Raillard, E. Bermudez and W.P.C. Stemmer (1998): "DNA shuffling of a family of genes from diverse species accelerates directed evolution", *Nature*, **391**, 288-291; and O. Kuchner and F. H. Arnold (1997): "Directed evolution of enzyme catalysts", *Trends in Biotechnology*, **15**, 523-530.

In an advantageous embodiment, the present method is used to engineer LTA_4 hydrolase inhibitors and/or analogues. In a specific embodiment of said method, a compound capable of mimicking the suicidal mode of LTA_4 hydrolase catalysis, thus acting as a mechanism-based suicide inhibitor, or otherwise capable of regulating the production of LTB_4 is engineered. In an alternative embodiment, an inhibitor of LTC_4 synthase or an LTB_4 receptor antagonist is designed.

2.4.8 (b) Novel specifically designed proteins

Further, the present invention also relates to any novel protein designed by use of the above described method. Once specified, such proteins may be produced by any conventional method well known to the skilled in this field, some of which are examplified below. In Example 2 below, the binding of hydroxamic acid to LTA4 hydrolase is discussed. Thus, such a modified hydroxamic is one example of a novel inhibitor specifically designed according to the invention, and the resoning in the

example may be used as a basis for the way of reasoning that is used in the present design.

Accordingly, novel enzymes may be produced, which are capable of any different chemical activity. For example, enzymes capable of novel catalytic properties, enzymes that in turn produce enzymes, etc., may be produced according to the present invention.

2.4.8 (c) Use of genetically modified LTA_4 hydrolase

The invention also encompasses the use of a genetically modified LTA4 hydrolase, obtained by any method according to the invention, with altered catalytic properties, e.g., increased ability to synthesize LTB4. The modified enzyme may thus be used for production of LTB4, or any analogues substances, a biomedical reagent which in turn may be used in, e.g., studies of leukotriene metabolism, induction of chemotaxis, as a reference compound in analysis of leukotrienes etc.

2.4.9 Pharmaceutical applications of the present invention

2.4.9 (a) First medical indication

Further, the invention also encompasses a compound obtainable by the method of screening LTA_4 hydrolase binding compounds, structure-based drug design, or the protein engineering methods described above, and more preferably, said compound for use as a medicament. One specifically advantageous embodiment is the herein disclosed novel M1 inhibitor for use as a medicament.

In an advantageous embodiment, the present compounds are used in the manufacture of a medicament for the treatment and/or prevention of acute and chronic inflammatory disorders, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis and chronic obstructive pulmonary disease (COPD); neoplasias and/or cancer; or disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax. Alternatively, the use may relate to the manufacture of a medicament for the treatment and/or prevention of an inflammatory and/or allergenic disorder, such as bronchial asthma, allergic rhinitis, conjunctivitis etc. Yet an alternative use is in the manufacture of a medicament for the treatment and/or prevention of infection caused be human immunodeficiency virus

(HIV). The novel M1 inhibitor are preferably used in medicaments for the treatment and/or prevention of such various diseases as cancer and/or endochrinological disturbances.

2.4.9 (b) Second medical indication and pharmaceutical methods

Thus, the present invention relates to the above mentioned molecules prepared by the method according to the invention for use in the manufacture of various medicaments for the above defined conditions. The invention also encompasses pharmaceutical preparations containing these molecules together with pharmaceutically acceptable carriers. Methods for the preparation of pharmaceutical preparations are e.g. found in Remington's Pharmaceutical Sciences, Mack Publishing Company, Philadelphia, PA, 17th ed. (1985). For a review of drug delivery, see Langer, Science 249:1527-1533 (1990). As those skilled in this field easily realise, the form of such a pharmaceutical preparation, the mode of administration thereof as well as suitable dosages will depend on the specific disease to be treated, the nature of the active substance used, the patient's age, body weight etc.

2.4.9 c) Methods of treatment

The present invention also encompasses any method of treatment for the above defined purposes. Exact details regarding such methods are determined by the practitioner depending on the specific circumstances from case to case.

2.5 Production of novel proteinaeous compounds

The compounds, which may be proteins, polypeptides, peptides or any other organic molecules, prepared according to the methods according to the invention may be synthesized chemically by methods well known to those of skill in this field or they may be prepared by use of recombinant DNA technology by any suitable method well known to those of skill in this field. General methods of synthesis are e.g. found in Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology, vol. 152, Academic Press, Inc., San Diego, CA; Sambrook et al., Molecular Cloning, A Laboratory Manual, 2nd Ed., vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989; and Current Protocols in Molecular Biology, F.M. Ausbel et al., Current Protocols (1994). Methods of reducing and denaturing proteins and inducing re-folding are well known to those of skill in the art,

see e.g. Debinski et al., J. Biol. Chem., 268: 14065-14070 (1993); Kreitman and Pastan, Bioconjug. Chem., 4: 581-585 (1993); and Buchner et al., Anal. Biochem., 205: 263-270 (1992).

2. 6 Detailed description of the drawings

Figure 1 shows key enzymes and intermediates in leukotriene biosynthesis.

Figure 2 shows 2Fo-Fc density contoured at 1.1 σ. Part of the active site in the neighborhood of the bestatin molecules is shown. Figures are created using a modified version of Molscript48,49.

Figure 3 is a ribbon diagram of the tertiary structure of LTA4 hydrolase. The N-terminal domain at the top of the diagram is rich in β-strands and connects to the catalytic domain to the left in the figure which is more α-helical and extends into the central part of the molecule. The C-terminal domain, illustrated at the bottom of the ribbon diagram, extends towards the right side of the catalytic domain.

Figure 4 (a) is a ribbon diagram of the N-terminal domain with its layers of β-strands, while (b) is a superimposition of the Cα trace of the N-terminal domain on the Cα trace of bacteriochlorophyll *a*. The N-terminal domain covers approx. half of the bacteriochlorophyll *a* structure (the right and bottom part of the diagram).

Figure 5 (a) is a ribbon diagram of the catalytic domain. In the center of the diagram, the three zinc binding ligands, His295, His299, and Glu318, as well as the inhibitor bestatin are depicted in ball and stick representation. The zinc ion is shown as a CPK model. The diagram in (b) shows the structure of thermolysin in the same orientation as the catalytic domain of LTA4 hydrolase. The three zinc ligands, His142, His146, and Glu166, as well as the inhibitor Cbz-GlyP-(O)-Leu-Leu50 are depicted in ball-and stick representation. The zinc ion is shown as a CPK model.

Figure 6 shows the structure of the C-terminal domain.

Figure 7 shows the zinc binding ligands in LTA4 hydrolase, His295, His299, and Glu318, superimposed on those in thermolysin, His142, His146, and Glu-166. Other catalytic or neighboring residues in the two enzymes are Tyr383, Glu325, Glu296, Thr302, and Asn317 in LTA4 hydrolase which correspond to His231, Asp170, Glu143, Asn165, and Tyr157 in thermolysin.

Figure 8 (a) is a Ball-and-Stick presentation of the binding of bestatin in LTA4 hydrolase.

Figure 8 (b) is a schematic overview of bestatin binding in LTA4 hydrolase.

Figure 9 (a) is a wire representation of the cavity found in LTA4 hydrolase (shown as Cα-trace).

Figure 9 (b) is a schematic presentation for the proposed binding of LTA4 into the cavity.

Figure 10 is a schematic representation for the proposed epoxide hydrolase reaction mechanism. The catalytic zinc acts as a Lewis acid and activates the epoxide to form a carbocation intermediate according to an S_N1 reaction. Water is added at C12 in a stereospecific manner, presumably directed by Asp375. The double bond geometry is controlled by the binding conformation of LTA4. Further details are given elsewhere in the present description.

3. EXPERIMENTAL

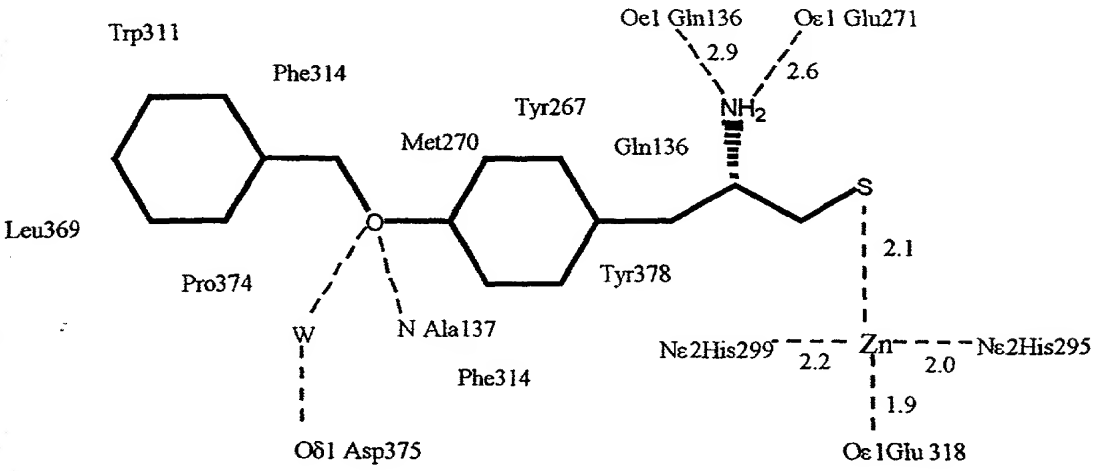
The following examples are intended for illustrating purposes only and should not in any way be used to construe the scope of the protection of the present invention as defined by the appended claims. All the references given below, and previously in this specification, are hereby included herein by reference.

3.1 Examples

Example 1: Binding of the thiol-compound (I)

The thiol group of the compound is ligated to the Zn^{2+} ion, that has a tetra-hedral configuration. Both the phenyl-groups are making extensive hydrophobic interactions. The first one makes aromatic stacking interactions with Phe314 and Trp311. Further hydrophobic interactions are made with Pro374 and Leu369. The other phenyl ring is making stacking interactions with Tyr267 and Tyr378. Met270 and Gln136 provide additional hydrophobic interactions. The ether-oxygen in the linker between the two phenyl rings makes a hydrogen bond to the backbone nitrogen of

Ala137 and also with a water molecule which is linked to Asp375. The amine group makes interactions to the Oε1 of Gln136 and the Oε1 of Glu271.

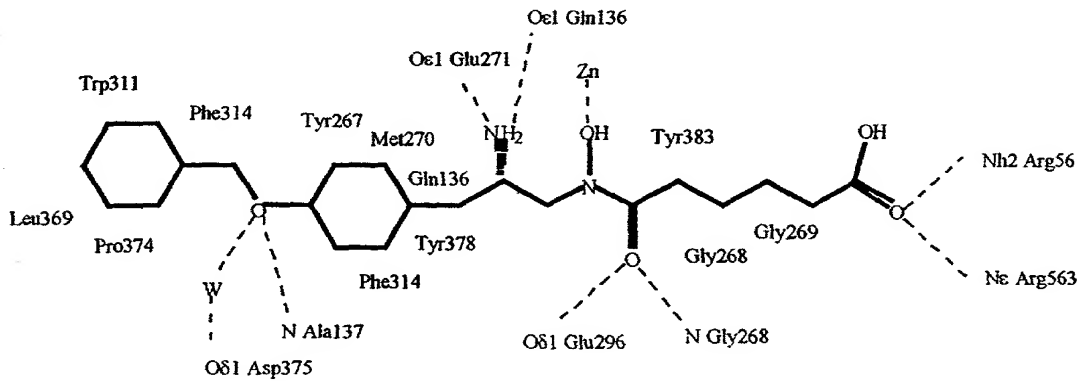


Formula (I)

Example 2: Binding of the hydroxamic acid compound (II)

The binding of this compound is very similar to the binding of the thiol compound described above. The manner in which the phenyl-moieties, the linker region and the amine group are bound is identical. The manner in which the hydroxamic acid part is bound is different in comparison with other complexes such as thermolysin-HA complexes and LTA_4-hydrolase-bestatin complex. Instead of a double interaction of the hydroxyl and carbonyl oxygens and the Zn ion resulting in a pentavalent co-ordination, here only one of the oxygens (the hydroxyl) is making an interaction with the Zn ion giving a tetrahedral co-ordination. The other oxygens make an interaction to Asp296 and the backbone nitrogen of Gly268. This difference is probably due to the tight binding of the phenyl rings and the amine group. The linkage between the amine group and the hydroxamic acid group contains one more carbon atom than in a normal or modified peptide-linkage. Since the binding site for substrates is rather narrow near the Zn ion, the conformation of compounds which bind in this area is rather restricted. Therefore one of the otherwise binding oxygens is pushed out and can no longer make an interaction with the Zn^{2+} ion. Removal of this extra

carbon atom could yield a compound which is a better inhibitor than this hydroxamic acid compound. The acid group at the other end of the compound is fixed by making a double interaction with the Nε and the Nh2 of Arg563.



Formula (II)

Example 3: Structure determination of two specific inhibitor-LTA_4 hydrolase complexes

Crystals, grown as described above, were soaked in 1 mM solution of thiolamine (Yuan et al., 1993) or 0.5 mM solution of hydroxamic acid (Hogg et al., 1995) in 15% PEG8000, 50 mM Imidazol pH 6.7, 25 mM acetate and 2.5 mM $YbCl_3$. After at least 24 hours, the crystals were transferred to a solution that contained a cryoprotectant (see above) and subsequently flash frozen in liquid nitrogen. The data for the crystal soaked with thiolamine was obtained at BM14B at the EMBL-outstation in DESY, Hamburg. The data for the hydroxamic acid was collected at beamline 7/11 at MAX-lab, Lund. Statistics from the data collections are shown in the table. The data were processed using MOSFLM, merging and other manipulations were performed by programs from CCP4 and the BIOMOL packages. The refinement procedures for both datasets were very similar. First rigid body refinement using TNT was performed. As a starting model for refinement and model building the structure of LTA4 hydrolase complexed with bestatin was used. The bestatin molecule and all water molecules were deleted from the model. After this initial refine-

ment it was possible to build the inhibitors into the protein. For evaluation of the density maps and model-building the program QUANTA (Molecular Simulations Inc., Burlington, MA) was used. The refinement was continued using TNT and was combined with sessions of model-building. In all rounds no sigma cut-offs were used and the resolution was slowly increased during the procedure. Water molecules were identified and incorporated into the models. During these procedures the R_{free} was carefully monitored. When refinement had converged, it was finished with one round in which all reflections, including those who were used for the calculations of the R_{free}, were incorporated. Statistics about refinement and quality of the models can be found in Table 5.

Table 8: Statistics of refinement and quality of the model

	Thiolamine (Thiol)	Hydroxamic acid (HA)
Resolution	15-2.5Å	15-1.8Å
Rfactor	17.8%	24.2%
Rfree	24.4	29.7%
Bond Lengths	0.011Å	0.012Å
Angles	1.9°	2.0°
Trigonal groups	0.005Å	0.006Å
Planar groups	0.009Å	0.010Å
Contacts	0.026Å	0.041Å
No. of waters	252	127

Example 4: Purification of LTA4 hydrolase.

For adsorption chromatography on hydroxyapatite, a TSKgel HA-1000 column (Tosohaas) was equilibrated in 10 mM potassium phosphate buffer, pH 7.1, supplemented with 0.2 mM $CaCl_2$. The enzyme sample was applied and a linear gradient of increasing phosphate (10 - 400 mM) was developed by mixing the starting buffer with 400 mM potassium phosphate buffer, pH 6.8, supplemented with 10 µM $CaCl_2$. Active fractions containing LTA4 hydrolase were eluted between 150 - 190 mM potassium phosphate.

Anion exchange chromatography was performed on a Mono-Q HR 5/5 column (Pharmacia Biotech) equilibrated with the loading buffer 10 mM Tris-Cl, pH 8. The pure protein was eluted using a linear gradient of KCl (0 - 500 mM) and was recovered at 110 - 140 mM KCl.

Example 5: Enzyme engineering

The present inventors have shown, that when Tyr-378 in LTA4 hydrolase was exchanged for a Phe residue, the resulting mutated enzyme was no longer suicide inhibited by LTA4 and exhibited a substantially increased catalytic efficiency. Furthermore, the mutated enzyme was capable of converting LTA4 not only into the natural product LTB4, but also into a novel metabolite, 6-*trans*-8-*cis*-LTB4. (Mueller, M.J., *et al. Proc Natl Acad Sci U S A* **93**, 5931-5935 (1996)).

Example 6: Enzyme-engineering

Tyr-383 in mouse LTA4 hydrolase was exchanged for Gln residue, which resulted in a mutated enzyme capable of forming the unnatural product 5S, 6S-dihydroxy-7,9-*trans*-11,14-*cis*-eicosatetraenoic acid from LTA4 (Andberg, M., Hamberg, M. & Haeggstrom, J.Z. *J. Biol. Chem.* **272**, 23057-23063 (1997)).

Example 7: Crystallisation of LTA_4 hydrolase

LTA_4 hydrolase was crystallised using $YbCl_3$ as an additive, 15% PEG and 50 mM Na-acetate as precipitant and 50 mM imidazole, pH 6.7, as buffer. Liquid-liquid-diffusion in capillaries were used as crystallisation set-ups.

3.2 Materials and Methods

Enzyme purification. Human recombinant LTA4 hydrolase was expressed in *E. coli* and purified to homogeneity in four chromatographic steps on FPLC using anion exchange, hydrophobic interaction, chromatofocusing, and hydroxyapatite resins, essentially as described (Wetterholm A., Medina J.F., Rådmark O., Shapiro R., Haeggström J.Z., Vallee B.L., Samuelsson B. Recombinant mouse leukotriene A4 hyd-

rolase: a zinc metalloenzyme with dual enzymatic activities. *Biochim. Biophys. Acta.* **1080**, 96-102 (1991)).

Crystallization conditions. The chemicals used for the crystallization experiments were purchased from Merck and were of highest purity available. The sparse matrix kit was obtained from Hampton Research. Crystallization conditions for the protein were initially sought by using the sparse matrix approach (Jancarik, J. & Kim, S.-H. J. Appl. Crystallogr. **24**, 409-411 (1991)) in hanging drop vapor diffusion set-ups in cell culture plates at room temperature. Under condition 28, (30% PEG8000, 0.2 M sodium-acetate, 0.1 M cacodylate buffer, pH 6.5) needles grew. They were subsequently reproduced and optimized using a finer grid search, different temperatures for the equilibration and testing of additives. Crystals were only obtained when the inhibitor bestatin was present in the crystallization set-ups. Using $YbCl_3$ as an additive and switching to liquid-liquid diffusion in capillaries, allowed plate-like crystals to grow. Thus, 5 µl 28% PEG8000, 0.1 mM Na-acetate, 0.1 mM imidazole buffer, pH 6.8, 5 mM $YbCl_3$ is injected into the bottom of a melting point capillary and an equal volume of LTA4 hydrolase (5 mg/ml) in 10 mM Tris-Cl, pH 8, supplemented with 1 mM bestatin, is layered on top. Finally, the capillary is closed and stored at 22°C. Crystals with an average size of 0.6 x 0.4 x 0.05 mm^3 appear in 3 to 4 weeks.

Crystal properties. The plate-like crystals diffract beyond 2Å using synchrotron radiation. They belong to space-group P21212 with cell dimensions a = 67.59 Å, b = 133.51 Å, c = 83.40 Å, a = b = g = 90 ° at 100K. As a cryo-solution, a mixture of 15%PEG 8000, 50 mM Na-acetate, 50 mM imidazole buffer, pH 6.8, 2.5 mM $YbCl_3$, and 25% glycerol was used. Assuming one molecule per asymmetric unit the solvent content of the crystals is 48%.

Structure determination. The structure was determined by using multiple anomalous dispersion measurements on the LIII edge of Ytterbium (λ = 1.3862 Å) at beam line BM14 at the European Synchrotron Radiation Facility (ESRF), Grenoble. Three datasets, peak (PK), point of inflection (PI) and remote (RM), were collected to 2.5Å resolution from the same crystal. The crystal was aligned such that Bijvoet

equivalent reflections could be collected in one pass of 90° for each wavelength. For RM a subsequent dataset to 2.15Å was collected. A second crystal was used for obtaining a dataset to 1.95Å. (For statistics on data-collection and quality, see table 1). Data were integrated using the program Denzo, scaled to each other using Scalepack (Otwinowski, Z. *Data collection and Processing. Proceedings of the ccp4 study weekend. SERC Daresbury Laboratory, Warrington, UK.* , 56-62 (1993)) and further analyzed using programs from the CCP4 package (Collaborative Computing Project Number 4. *Acta Crystallogr. Sect. D* **50**, 760-763 (1994)).

From Patterson functions one major and one minor Yb position could readily be identified, a third position was identified during heavy atom refinement in difference Fourier maps. The heavy atom parameters were refined using MLPHARE (Otwinowski, Z. *Isomorphous replacement anomalous scattering. Proceedings of the CCP4 study weekend. SERC Daresbury Laboratory, Warrington, UK.* , 80-85 (1991)) and SHARP (de La Fortelle, E. & Bricogne, G. *Met. Enzymol.* **276**, 472-494 (1997)). The final figures of merit was 0.57 to 2.15Å. Phase information was further improved to 2.15Å by solvent flattening using SOLOMON (Abrahams, J.P. & Leslie, A.G.W. *Acta Crystallographica* **D52**, 30-42 (1996)) with a solvent content of 43%. The quality of the maps was very good and the entire protein molecule (residue 1-610) could be traced unambiguously. All model building was performed using QUANTA (Molecular simulations). Refinement was started by a run of slow-cooling molecular dynamics in XPLOR (Brünger, A.T., Kuriyan, J. & Karplus, M. *Science* **235**, 458-460 (1987)) using the RM dataset to 2.7Å. The three Yb ions were included into the refinement with full occupancy for the first Yb and half occupancy for the two other ions. All subsequent refinement was performed with TNT (Tronrud, D.E., ten Eyk, L.F. & Matthews, B.W. *Acta Crystallogr. Sect. A* **43**, 481-501 (1987)). The same set of reflections (4% of total amount from 25-1.95Å) for the calculation of R_{free} (Brünger, A.T. *Nature* **355**, 472-475 (1992)) was maintained throughout all refinement procedures. The resolution was slowly improved by alternating sessions of model-building and refinement. The data for the second crystal to 1.95Å were used for further refinement during which a Zn ion, bestatin, an acetate

and an imidazole molecule were identified. Judged from the B-factors these molecules are all fully occupied. 540 water molecules were added to the coordinates. The R_{free} was 24.7% and the working R-factor was 18.8% for all data between 25-1.95 Å. In a final round of refinement all data between 25-1.95 Å were included, yielding a final R-factor of 18.5 % for residues 1-610, 3 Yb ions, 1 Zn, 1 bestatin, 1 imidazole, 1 acetate and 540 water molecules. Most of the model is in good density (Fig. 2) except a loop encompassing residues 179 to 184 for which only poor density was obtained. The model has good stereo-chemical parameters (r.m.s bonds =0.010Å, r.m.s angles = 2.2°) and 91.7% of the residues lie in the most favored part of the Ramachandran plot.

4. RESULTS AND DISCUSSION

4.1 Overall structure and domain organization

The leukotriene A4 hydrolase molecule is folded into three domains; an N-terminal domain, a catalytic domain and a C-terminal domain which together form a flat triangular arrangement with approximate dimensions of 85 x 65 x 50 $Å^3$. The overall structure of the enzyme is depicted in figure 3. Although the three domains pack closely and make contact with each other, a deep cleft is formed in between.

4.2 The N-terminal domain is structurally related to bacteriochlorophyll *a*

The N-terminal domain (residue 1-209) is composed of one 7 stranded mixed b-sheet, one 4 and one 3 stranded antiparallel β-sheet. Strands from the larger β-sheet continue into the two smaller β-sheets that pack on the edges of the same side of the larger sheet so that a kind of envelope is formed (Fig. 4a & b). The two small β-sheets are turned towards the inside of the whole protein while the larger β-sheet is exposed to solvent and forms a large concave surface area. Loops connecting the other strands and hydrophobic residues fill the core of this domain. The N-terminal domain of LTA4 hydrolase shares important structural features with the chlorophyll-containing enzyme bacteriochlorophyll (Bchl) *a* (Matthews, B., Fenna, R., Bolognesi, M., Schmid, M. & Olson, J. *J. Mol. Biol.* **131**, 259-285 (1979)). Thus, 111 Cα positions have equivalent positions in the two proteins despite the absence

of any sequence identity (Fig. 4b). The domain is about half the size of Bchl *a* which has a single domain structure without major extensions. Like Bchl *a*, the shape of the N-terminal domain resembles an envelope (or Taco) with a hollow inside and in Bchl *a*, 7 bacteriochlorophylls are buried in this cavity. However, the domain is not as hollow as BChl *a* since loop 135-155, which contains a small helical segment, is turned inwards and fills up the core. In BChl *a* the equivalent loop (290–305) is positioned more towards the exterior of the protein, thereby leaving space for some of the tertrapyrroles of the bacteriochlorophylls. The large sheet (17 strands) of Bchl *a* is truncated to only 7 strands in LTA4 hydrolase. Especially the region between residue 35 and 263 of Bchl *a* has been replaced by a much shorter region in LTA4 hydrolase (res. 45 to 98) that forms the 3 stranded small β-sheet and the edge strand of the larger 7 stranded β-sheet. The structure of the other half of the molecule is almost completely conserved, except the insertion of two extra strands instead of loops in LTA4 hydrolase. The structural homology between Bchl *a*, a protein involved in light harvesting, and LTA4 hydrolase was certainly unexpected. In LTA4 hydrolase, the function of the N-terminal domain is not yet known, but one may speculate that it participates in binding to hydrophobic molecules or surfaces with a possible regulatory function. In mammalian 15-lipoxygenase, a similar function was proposed for an N-terminal β-barrel domain with structural homology to a corresponding C-terminal domain in mammalian lipases (Gillmor, S.A., Villasenor, A., Fletterick, R., Sigal, E. & Browner, M.F. *Nature Struc. Biol.* 4, 1003-1009 (1997)).

The connection from the N-terminal to the catalytic domain is very short, a strand from the 4 stranded β-sheet connects into a strand of a 5-stranded antiparallel β-sheet of the catalytic domain. The two sheets are closely packed and the interface is mainly hydrophobic in character with 14 hydrophobic residues contributing from the N-terminal domain and 11 from the catalytic domain. Hydrogen bonds occur between Gln116 and Ser264, Ser124 and Gln226, the backbone of Ser124 and Glu223, the backbone of Ser151 and Lys309, Lys153 and the backbone of Leu305 and indirectly through a water molecule between Tyr130 and the back-

bone of Val260. Two salt-bridges between His139 and Asp375 and between Arg174 and Asp257 complete the interactions made in this interface.

4.3 The catalytic domain contains the zinc binding site and is structurally similar to thermolysin

The structure of the catalytic domain (res. 210-450) is surprisingly similar to the structure of thermolysin (Fig. 5a & b) (Holmes, M. & Matthews, B. *J. Mol. Biol.* **160**, 623-639 (1982)). When the amino acid sequence in this domain was compared with that of thermolysin, the sequence identity was found to be very low (essentially confined to the zinc binding motifs). However, the structural homology stretches out over the whole domain. Thus, no less than 146 Ca positions overlap with an r.m.s. deviation of 1.946 Å. Like thermolysin, the catalytic domain consists of two lobes, one mainly a-helical and one mixed a/b lobe. The a-lobe consists of 6 major helices interconnected by long loops containing smaller helical segments, while the a/b lobe has a 5 stranded mixed β-sheet lined with 3 helices on one side. The zinc binding site is found in between the two lobes. Since this domain contains only 245 amino acids and thermolysin contains 314 residues, some truncations have taken place, especially in the a/b lobe in which the N-terminal extended b structure is truncated and only a mixed 5 stranded β-sheet remains. The changes in the a-lobe are smaller. Here the long meandering loop 181 to 221 has been replaced by a long a-helix and the b-hairpin from 245 to 258 has been deleted.

A loop in extended conformation on the surface of the protein from 451 to 463 connects the catalytic domain with the C-terminal domain. Interestingly, this segment contains a highly conserved proline rich motif P451-G-f-P-P-x-K-P-x-Y460 which bears some resemblance to an SH3 domain recognition sequence. However, the canonical arginine residue is not present on either side of the proline motif. Nevertheless, since this stretch of amino acids is exposed on the surface of the protein, it is still possible that it could serve as an anchoring site for protein-protein interactions.

The C-terminal domain (464-610) is composed of 9 a-helices that form an unusual coil of helices reminiscent of the ones found in lytic transglycosylase[40] and

recently in the armadillo repeat region of b-catenin (Huber, A.H., Nelson, W.J. & Weis, W.I. *Cell* **90**, 871-882 (1997)) (Fig. 6). The helices pack into two layers of parallel helices (5 inner and 4 outer helices) and in an anti-parallel manner between the two layers. The arrangements found in the two other proteins are much larger and form super-helical structures. In the C-terminal domain of LTA4 hydrolase, the arrangement is more straight and has a very compact shape. One of the helices is deformed and one of the interconnecting loops is long and contains a small 310 helix. The domain makes contacts with both the a-lobe of the catalytic domain and one of the edges of the N-terminal domain. It is positioned in a way such that the helices lie perpendicular to the 7 stranded b-sheet of the N-terminal domain and to most of the helices in the catalytic domain. The helices are amphipatic in character, with the hydrophobic sides towards the middle of the domain and hydrophilic residues pointing towards the solvent and into the deep cleft in the middle of the whole molecule. This side of the cleft is highly polar; 10 Arg and Lys residues and 4 Asp and Glu residues are positioned on this side.

4.4 Zinc coordination

The immediate surroundings of the active site Zn^{2+} ion are very similar in thermolysin and LTA4 hydrolase. The Zn^{2+} is bound between the two lobes and is coordinated by His295, His299, one carboxylic oxygen of Glu318 and the carbonyl and hydroxyl oxygens of the inhibitor bestatin so that a square based pyramid is formed. The two histidines originate from a long a-helix and the glutamate from a neighboring a-helix, all in the a-lobe. Glu296 and Tyr383, two residues implicated in the reaction mechanism for the peptide cleaving activity, are located near the Zn ion. Glu296, the putative general base, is positioned next to the metal ligand His295 and bends over the bestatin molecule and Tyr383, which was described as a proton donor, also makes contact with the bestatin molecule (Figure 8a).

Interestingly, the second layer around the Zn ion shows differences between thermolysin and LTA4 hydrolase. In both enzymes the orientation of the zinc binding ligands is fixed by hydrogen bonds, however the hydrogen bond acceptors are positioned differently. In thermolysin, the Nd1 of His142 is hydrogen bonded to the

Od2 of Asp170, while in LTA4 hydrolase the Nd1 of His295 is hydrogen bonded to the Oe1 of Glu325. This residue comes from a structural equivalent to the helix carrying Asp170 in thermolysin, but is shifted half a turn outwards. The Nd1 of His146 in thermolysin is hydrogen bonded to the Od1 of Asn165. This residue is part of the zinc binding signature and is conserved between the two enzymes. However, in LTA4 hydrolase the helix in which this conserved residue is placed has been rotated slightly and Asn317 is no longer making a hydrogen bond to His299. The orientation of His299 is now fixed by a hydrogen bond from the Nd1 to the carbonyl backbone oxygen of Thr302. The Od1 of Asn317 makes instead a hydrogen bond to the backbone amide of Asn381 while the Nd2 makes a hydrogen bond to the hydroxyl group of Tyr200. The last protein-ligand, Glu166 is in thermolysin hydrogen bonded to Tyr157 and a water molecule, in LTA4 hydrolase, Glu318 is only hydrogen bonded to a water molecule (Fig. 7).

4.5 Bestatin binding

Although the zinc binding site is formed by residues only from the catalytic domain and most catalytic residues also come from this domain, the active site itself is surrounded by loops from all three domains. The binding of bestatin reflects this, since it makes interactions with residues from all three domains. The main interactions of bestatin are made through the carbonyl and hydroxyl oxygens to the Zn atom. Hydrophobic interactions are made between the phenyl moiety and the phenyl rings of Tyr267, Phe316, Tyr378 and Tyr383. Also, Met270 and Gln136 are involved (Fig. 8a). The other end of the inhibitor is pointing towards the solvent, the leucine moiety makes interactions with Val292 and His295, while the carboxylic oxygens make interactions with Arg563 and Lys565 through water molecules as well as hydrogen bonds to the backbone nitrogen atoms of Gly268 and Gly269. Hydrogen bonds are formed between the peptidyl N of bestatin and Oe2 of Glu296 and between the terminal NH_2 and the Oe1 of Glu271 and Oe1 of Gln136. The hydroxyl oxygen makes apart from the interaction with the Zn ion also an interaction to the OH of Tyr383. (For schematic overview see Fig. 8b). Tyr378 which gets modified during suicide inactivation sits slightly further away, but makes a hydro-

gen bond to Tyr383 and some hydrophobic interactions with the phenyl ring of the inhibitor. These two tyrosine are both found on the same stretch of amino-acids that in thermolysin form a long a helix, however in leukotriene hydrolase this helix is interrupted and two turns of the helix are replaced by three residues (378-380) in an extended conformation. The binding of bestatin is quite different as was found in the complex between bestatin and bovine lens leucine amino-peptidase (blLAP) (Burley, S., David, P., Sweet, R., Taylor, A. & Lipscomb, W. *J. Mol. Biol.* **224**, 113-140 (1992)). In that complex, bestatin was bound to the Zn by both the terminal nitrogen and the nonproteinaceous P1 hydroxyl oxygen, while in LTA4 hydrolase the bestatin is bound by the hydroxyl and carbonyl oxygens. The terminal nitrogen is involved in hydrogen bonding to Glu271 and Gln136. These differences could stem from the fact the blLAP is a bimetal protein with a different reaction mechanism. Moreover the binding of bestatin as seen in LTA4 hydrolase is similar with the complexes formed between thermolysin and hydroxamates which also act as bidentate ligands by the hydroxyl and carbonyl oxygens (Holmes, M. & Matthews, B. *Biochemistry* **20** (1981)).

Behind the pocket in which the phenyl ring of bestatin binds, there is a cavity that stretches 15 Å deeper into the protein and is approximately 6 to 7 Å wide. In the present structure this cavity is filled with water molecules. It has however a very hydrophobic nature and is lined with Trp311, Phe314, Trp315 Phe362, Leu365, Val367, Leu369, Pro374, Ala377, Tyr378, and Pro382. Most of these residues are strictly conserved or conserved in nature in all LTA4 hydrolase sequences known up until now, with the exception of Val367, which is replaced by a Gln in the yeast and *C. elegans* sequences. Interestingly space for this cavity is partly created by the interruption by the extended conformation in the stretch where Tyr378 and Tyr383 are found. One patch of this binding site is quite hydrophilic with Asn134, Asp375 and the OH of Tyr267 clustering together. This bigger cavity could be a binding site for the LTA4 substrate molecule. If the epoxide moiety would bind in a similar way as the carbonyl oxygen of bestatin to the Zn ion, then the hydrophobic tail would fit snugly into the binding site now occupied by the phenyl group of bestatin and

would continue into the deeper hydrophobic cavity (Fig. 9a). The other tail would sit in the pocket that is now occupied by the carboxy group of bestatin and it would be long enough for the carboxylic acid to make direct electrostatic interactions with the conserved Arg563 and Lys565.

The replacement of Val367 by Gln as seen in the enzyme from yeast would make the hydrophobic channel shorter and this might be one of the reasons why the yeast enzyme has a poor leukotriene A4 epoxide hydrolase activity. The manner in which the leukotriene molecule would bind is similar as what is proposed for binding of arachidonic acid in 15-lipoxygenase (Gillmor, S.A., Villasenor, A., Fletterick, R., Sigal, E. & Browner, M.F. *Nature Struc. Biol.* 4, 1003-1009 (1997)) with the hydrophobic end buried inside the protein and the carboxylic acid more towards the surface making interactions with Arg and Lys residues.

The binding of bestatin acts also as a guide for the binding of peptide substrate molecules. From systematic binding studies with tri-peptides it was shown that the enzyme has a strong preference for an arginine residue as the N-terminal residue and for several tri-peptides the enzyme has a kcat/Km ratio 10-fold the kcat/Km for LTA4 (Örning, L., Gierse, J.K. & Fitzpatrick, F.A. *J. Biol. Chem.* 269, 11269-11273 (1994). If we roughly model a peptide in the active site with an N-terminal Arg with the carbonyl oxygen sitting on the place of the hydroxyl group of bestatin, then the Arg side-chain of this residue would sit in the same place as the phenyl group of the bestatin with the guanidinium headgroup interacting with the conserved Asp375 and the OH of Tyr267 and the more hydrophobic Cb, Cd and Cg atoms making similar interactions as the phenyl ring. The terminal aminogroup could make the same electrostatic interaction as the terminal aminogroup of bestatin with Asp271 and Gln136. This mode of binding of bestatin is in contrast with the mode proposed by Örning, since the phenyl ring seems to occupy the S1 pocket. We also propose that the LTA4 substrate molecule is occupying all three pockets, S1, S'1 and S'2.

If the binding mode of peptides in LTA4 hydrolase is compared with the one described for thermolysin, a number of differences are observed. In thermolysin, the

peptide molecule is held in place by many interactions to the main chain atoms provided by Asn112, Ala203, Arg203 and Trp115. None of these residues or equivalent residues can be found in the binding site in LTA4 hydrolase. Furthermore, although binding pockets S1 and S'1 are at similar positions as in thermolysin, site S'2 has to be different since its space is occupied by Tyr378 in LTA4 hydrolase. Glu271 and Gln136 and the N-terminal domain are filling up the space into which in thermolysin the upstream peptide binds contributing to the exo-peptidase function instead of an endo-peptidase function as in thermolysin.

4.6 Putative Phosphorylation site

Recently specific phosphorylation by a yet unknown specific kinase of Ser415 has been described as means of regulation of LTA4 hydrolase activity in endothelial cells (Rybina, I.V., Liu, H., Gor, Y. & Feinmark, S.J. *J Biol Chem* **272**, 31865-71 (1997)). This residue is conserved in all mammalian LTA4 hydrolases and is embedded in a highly homologous stretch of residues. Phosphorylation of this residue seems to inhibit the epoxide hydrolase activity but not the amino-peptidase activity. In the structure this residue is located in a loop connecting two a-helices that lie on the surface of the molecule. The loop itself is located at the back of the enzyme.

4.7 Aminopeptidase activity

The amino-peptidase activity catalyzed by this enzyme has been well studied and many of the important residues have been target for site-directed mutagenesis work. This lead to a proposal in which Glu296 would act as a general base (Wetterholm, A., *et al. Proc Natl Acad Sci U S A* **89**, 9141-9145 (1992)) and Tyr383 as a putative proton donor (Blomster, M., Wetterholm, A., Mueller, M.J. & Haeggström, J.Z. *Eur. J. Biochem.* **231**, 528-534 (1995)). In the current complex, these residues are involved in hydrogen bonds with the bestatin molecule. If bestatin binding is seen as a rough analog for the transition state binding, then the interaction of Glu296 with the hydroxyl oxygen of bestatin indicates that this residue could indeed activate a water-molecule for the nucleophilic attack. The role of Tyr383 cannot so easily be confirmed, however its position strongly suggest the role of proton donor. In thermolysin the proton donor is His231 and although the Ca position of this resi-

due is 4.1Å removed from the Ca position of Tyr383 in LTA4 hydrolase, the Nd1 is only 1 Å removed from the OH position of Tyr383. The conserved Glu271 could be involved in the exo-protease activity of the protein. Recently, the analogous Glu350 in aminopeptidase N and Glu352 in aminopeptidase A were subject to site-directed mutagenesis work (Luciani, N., *et al. Biochemistry* **37**, 686-692 (1998); and Vazeux, G., Iturrioz, X., Corvol, P. & Llorenz-Cortez, C. *Biochem. J.* **334**, 407-413 (1998)) and it was observed that mutations of this residue lead to large decreases in the activity in the case of substitutions by conserved amino-acids such as aspartate and glutamine and absence of activity in substitution by alanine. It was concluded that Glu350 belonged to the anionic binding site in that protein. A mechanism based on thermolysin was proposed for aminopeptidase N with a pentavalent transition state with an additional interaction between the free a-aminogroup and Glu350. In this structure we can observe such an interaction between Glu271 and the free aminogroup of bestatin. Furthermore the penta-valent coordination of Zn by the His295, His299, Glu318 and the carbonyl and hydroxyl groups of bestatin indicates that this is an equivalent transition state analog complex as determined previously for thermolysin.

From careful sequence alignments and structural insight we can conclude that the enzymes in the M1 family of proteases will share a highly conserved catalytic domain that includes part of the N-terminal domain as we see it in LTA4 hydrolase and the thermolysin-like domain. There is no homology for residues in the C-terminal domain and we believe that this domain is unique for LTA4 hydrolases. According to the present invention, it is suggested that all proteases belonging to class M1 with the signature HExxH and a Glu 18 residues downstream will function in a similar way to thermolysin.

4.8 Epoxide hydrolase activity

Concerning the epoxide hydrolase activity, much less is known about the functional elements and mechanisms of catalysis. In fact, the prosthetic zinc is the only critical component identified thus far and may potentially assist in the introduction of a water molecule at C12 or in the activation of the epoxide. Although Tyr378 and

Tyr383 are important active side residues, none of them is essential for catalysis. A mutation of Tyr378 to Phe protects the enzyme against suicide inhibition, however the specificity of the double bond configuration is partly lost (Mueller, M., Andberg, M., Samuelsson, B. & Haeggstrom, J. *J. Biol. Chem.* **271**, 24345-24348 (1996)) since a novel metabolite with a cis-trans-cis conjugated system can be detected. Thus, Tyr378 is a major binding site for LTA4 during suicide inactivation and seems to play a role for the formation of the correct double bond geometry in the product LTB4. Mutations of Tyr383 abolish the amino-peptidase activity where it has a role as potential proton donor (*vide supra*) but the epoxide hydrolase activity is only decreased compared to wild-type. It is however implicated in the stereospecific introduction of water during the hydrolysis of LTA4 to LTB4 since these mutants convert LTA4 in both LTB4 and 5 [S],6 [S]-DHETE (Andberg, M., Hamberg, M. & Haeggstrom, J. *J. Biol. Chem.* **272**, 23057-23063 (1997)). Moreover careful analysis of the catalytic properties of enzymes mutated in pos. 383, *viz* [Y383F], [Y383H] and [Y383Q]LTA4 hydrolase have indicated that the epoxide hydrolase reaction follows an SN1 mechanism.

If one considers the chemistry carried out by LTA4 hydrolase, the enzyme has two major tasks during the hydrolysis of LTA4 to LTB4. First introduction of a water molecule stereospecific at C12 and second to generate a *cis*-double bond Æ6 in the resulting conjugated triene system [cf. Fig. 1]. If LTA4 is modeled into the putative substrate binding pocket as indicated in figure 9b, the catalytic zinc gets close to the epoxide and not C12 of the substrate. Therefore the most likely role of the Zn ion is to act directly as a Lewis acid to activate and open the epoxide ring. This would generate a carbocation, whose charge will be delocalised over the conjugated triene system from C7 to C12. Since this intermediate has an *sp2* hydridized planar configuration at C12, it is in principle open for nucleophilic attack from either side of the molecule. The conserved Asp375 is positioned in such a way that a water molecule bound to it is in "attacking" distance of C12 of a modeled LTA4 molecule, the position into which a hydroxyl group is inserted during the reaction.

This will account for the proper stereo-chemical and positional insertion of the hydroxyl-group at C12 in *R* configuration.

The shape and curvature of the LTA4 binding pocket also gives a clue as to how the enzyme creates the *cis* double bond at Æ6. Since there is free rotation between the c6 and c7 of LTA4, this bond may be kept in a "pro-cis" configuration in the transition state, which in turn would facilitate the formation of a *Æ6-cis* double bond form the carbocation intermediate. If LTA4 is modeled in this way, the entire molecule adopts a bent shape, fitting very well with the architecture of the binding pocket (Fig. 9b). Hence, the critical double bond geometry at Æ6 of LTB4 is probably guaranteed by the exact binding conformation of LTA4 at the active side which in turn is governed by all the structural elements participating in substrate binding, including the carboxylate recognition sites, Arg56 and Lys565, the catalytic zinc and the hydrophobic residues lining the pocket. The putative binding cleft for the leukotriene molecule is narrow and bend and thereby favoring LTA4 over other epoxides. The two tyrosines are positioned such that they are in contact with the triple double bond configuration of a modeled LTA4 molecule at the bent of the putative binding pocket and they are hydrogen-bonded to each other. Therefore their position is ideal for guidance in stereo-specificity of the double bond configuration. The loss of specificity for the hydroxyl-incorporation at the C12 position in case of the Tyr383 position can be explained that mutations at this position would possibly create extra space for a water molecule that could attack at the C6 position and thereby form 5 [S],6 [S]-DHETE.

The position of Tyr378 is such that it is in contact with the C6 atom of the modeled LTA4 molecule. If after opening of the epoxide ring the hydroxyl group of Tyr378 instead of a water molecule would attack the carbon-cation at the C6 position, a covalently attached molecule is formed which forms the suicide inhibited complex. In order to check this hypothesis and to obtain more information about the binding-site for leukotriene A4, the structure of this inhibited species would be essential.

In order to exclude the possibility that residues near the active site might have further catalytic roles in the epoxide hydrolase reaction, a thorough investigation of these residues, such as Glu271 and Gln136 has to be started. Furthermore the proposed role of Asp375 in activating a water molecule for the stereospecific attack at C12 has to be investigated.

Accordingly, the present invention has solved the first specific leukotriene converting enzyme, which for the first time reveals the binding mode for leukotriene molecules. Furthermore, insight is provided in a unique active site that harbours two activities using different amino-acids to catalyze different reactions.

5. CONFORMATIONAL DATA

Table 9: Structure coordinates of LTA_4 hydrolase-thiolamine complex

```
CRYST    68.560  132.150   83.270  90.00  90.00  90.00 P21212
SCALE1       0.01459   0.00000   0.00000        0.00000
SCALE2       0.00000   0.00757   0.00000        0.00000
SCALE3       0.00000   0.00000   0.01201        0.00000

          Atom res. Chain No.    x       y       z       occ   B-factor
ATOM      1  N   PRO A   1      -0.593  16.387  63.494  1.00 97.99
ATOM      2  CA  PRO A   1      -1.890  16.918  63.874  1.00 97.22
ATOM      3  C   PRO A   1      -2.210  18.371  63.525  1.00100.00
ATOM      4  O   PRO A   1      -2.402  18.667  62.342  1.00100.00
ATOM      5  CB  PRO A   1      -2.130  16.551  65.332  1.00 97.81
ATOM      6  CG  PRO A   1      -1.221  15.355  65.583  1.00100.00
ATOM      7  CD  PRO A   1      -0.290  15.233  64.369  1.00 97.05
ATOM      8  N   GLU A   2      -2.216  19.272  64.556  1.00 96.95
ATOM      9  CA  GLU A   2      -2.569  20.678  64.314  1.00 95.71
ATOM     10  C   GLU A   2      -2.188  21.701  65.386  1.00 94.33
ATOM     11  O   GLU A   2      -2.512  21.542  66.562  1.00 93.21
ATOM     12  CB  GLU A   2      -4.105  20.768  64.214  1.00 97.26
ATOM     13  CG  GLU A   2      -4.587  21.732  63.125  1.00100.00
ATOM     14  CD  GLU A   2      -4.351  21.139  61.767  1.00100.00
ATOM     15  OE1 GLU A   2      -3.301  21.261  61.152  1.00100.00
ATOM     16  OE2 GLU A   2      -5.361  20.398  61.368  1.00100.00
ATOM     17  N   ILE A   3      -1.550  22.799  64.944  1.00 86.29
ATOM     18  CA  ILE A   3      -1.148  23.905  65.820  1.00 81.53
ATOM     19  C   ILE A   3      -2.006  25.154  65.661  1.00 75.68
ATOM     20  O   ILE A   3      -2.835  25.288  64.763  1.00 76.97
ATOM     21  CB  ILE A   3       0.308  24.324  65.707  1.00 83.45
ATOM     22  CG1 ILE A   3       0.452  25.521  64.759  1.00 83.63
ATOM     23  CG2 ILE A   3       1.198  23.160  65.300  1.00 84.76
ATOM     24  CD1 ILE A   3      -0.184  25.361  63.375  1.00 91.36
ATOM     25  N   VAL A   4      -1.725  26.099  66.523  1.00 61.54
ATOM     26  CA  VAL A   4      -2.477  27.303  66.482  1.00 56.32
ATOM     27  C   VAL A   4      -1.658  28.552  66.623  1.00 50.98
ATOM     28  O   VAL A   4      -0.803  28.694  67.512  1.00 47.84
ATOM     29  CB  VAL A   4      -3.514  27.318  67.595  1.00 58.99
ATOM     30  CG1 VAL A   4      -3.735  28.754  68.047  1.00 58.40
ATOM     31  CG2 VAL A   4      -4.819  26.691  67.131  1.00 58.56
ATOM     32  N   ASP A   5      -2.012  29.486  65.732  1.00 39.38
ATOM     33  CA  ASP A   5      -1.403  30.782  65.763  1.00 32.64
```

ATOM	34	C	ASP	A	5	-2.308	31.596	66.634	1.00	36.35
ATOM	35	O	ASP	A	5	-3.343	32.051	66.171	1.00	38.30
ATOM	36	CB	ASP	A	5	-1.252	31.492	64.400	1.00	30.79
ATOM	37	CG	ASP	A	5	-0.251	32.581	64.563	1.00	29.96
ATOM	38	OD1	ASP	A	5	-0.069	33.123	65.635	1.00	35.01
ATOM	39	OD2	ASP	A	5	0.457	32.831	63.493	1.00	29.81
ATOM	40	N	THR	A	6	-1.931	31.745	67.903	1.00	32.32
ATOM	41	CA	THR	A	6	-2.710	32.507	68.842	1.00	32.08
ATOM	42	C	THR	A	6	-2.701	34.011	68.557	1.00	40.63
ATOM	43	O	THR	A	6	-3.484	34.759	69.132	1.00	46.68
ATOM	44	CB	THR	A	6	-2.357	32.171	70.295	1.00	44.71
ATOM	45	OG1	THR	A	6	-0.967	32.322	70.505	1.00	51.05
ATOM	46	CG2	THR	A	6	-2.789	30.741	70.604	1.00	35.79
ATOM	47	N	CYS	A	7	-1.842	34.480	67.656	1.00	32.51
ATOM	48	CA	CYS	A	7	-1.797	35.923	67.335	1.00	28.92
ATOM	49	C	CYS	A	7	-2.627	36.329	66.129	1.00	31.49
ATOM	50	O	CYS	A	7	-2.780	37.523	65.875	1.00	25.42
ATOM	51	CB	CYS	A	7	-0.362	36.410	67.107	1.00	27.38
ATOM	52	SG	CYS	A	7	0.686	35.944	68.518	1.00	32.02
ATOM	53	N	SER	A	8	-3.140	35.315	65.383	1.00	34.03
ATOM	54	CA	SER	A	8	-3.940	35.508	64.158	1.00	32.97
ATOM	55	C	SER	A	8	-5.410	35.136	64.264	1.00	33.52
ATOM	56	O	SER	A	8	-5.744	34.137	64.866	1.00	32.89
ATOM	57	CB	SER	A	8	-3.363	34.754	62.980	1.00	34.07
ATOM	58	OG	SER	A	8	-4.017	35.182	61.798	1.00	36.65
ATOM	59	N	LEU	A	9	-6.289	35.921	63.635	1.00	30.79
ATOM	60	CA	LEU	A	9	-7.724	35.649	63.672	1.00	31.91
ATOM	61	C	LEU	A	9	-8.198	35.009	62.377	1.00	36.07
ATOM	62	O	LEU	A	9	-9.359	34.626	62.216	1.00	38.61
ATOM	63	CB	LEU	A	9	-8.514	36.958	63.874	1.00	32.47
ATOM	64	CG	LEU	A	9	-8.306	37.688	65.212	1.00	35.39
ATOM	65	CD1	LEU	A	9	-9.113	38.983	65.193	1.00	32.27
ATOM	66	CD2	LEU	A	9	-8.746	36.816	66.397	1.00	33.25
ATOM	67	N	ALA	A	10	-7.273	34.933	61.443	1.00	28.63
ATOM	68	CA	ALA	A	10	-7.545	34.408	60.147	1.00	27.14
ATOM	69	C	ALA	A	10	-7.643	32.921	60.090	1.00	34.34
ATOM	70	O	ALA	A	10	-7.296	32.173	61.005	1.00	37.34
ATOM	71	CB	ALA	A	10	-6.551	34.936	59.100	1.00	27.72
ATOM	72	N	SER	A	11	-8.130	32.503	58.959	1.00	32.08
ATOM	73	CA	SER	A	11	-8.256	31.115	58.708	1.00	32.03
ATOM	74	C	SER	A	11	-6.838	30.519	58.656	1.00	32.67
ATOM	75	O	SER	A	11	-5.927	31.028	57.986	1.00	29.29
ATOM	76	CB	SER	A	11	-9.013	30.934	57.401	1.00	38.42
ATOM	77	OG	SER	A	11	-10.391	30.728	57.648	1.00	44.17
ATOM	78	N	PRO	A	12	-6.651	29.440	59.387	1.00	29.14
ATOM	79	CA	PRO	A	12	-5.370	28.786	59.476	1.00	26.83
ATOM	80	C	PRO	A	12	-4.935	28.176	58.173	1.00	32.64
ATOM	81	O	PRO	A	12	-5.737	28.007	57.284	1.00	35.89
ATOM	82	CB	PRO	A	12	-5.544	27.698	60.540	1.00	28.28
ATOM	83	CG	PRO	A	12	-7.029	27.571	60.843	1.00	32.92
ATOM	84	CD	PRO	A	12	-7.731	28.587	59.952	1.00	30.42
ATOM	85	N	ALA	A	13	-3.645	27.836	58.063	1.00	30.63
ATOM	86	CA	ALA	A	13	-3.066	27.236	56.855	1.00	28.36
ATOM	87	C	ALA	A	13	-3.644	25.852	56.576	1.00	33.99
ATOM	88	O	ALA	A	13	-3.455	25.240	55.528	1.00	31.60
ATOM	89	CB	ALA	A	13	-1.561	27.133	57.050	1.00	27.68
ATOM	90	N	SER	A	14	-4.338	25.352	57.571	1.00	31.10
ATOM	91	CA	SER	A	14	-4.919	24.069	57.469	1.00	30.66
ATOM	92	C	SER	A	14	-6.242	24.133	56.753	1.00	37.86
ATOM	93	O	SER	A	14	-6.768	23.118	56.328	1.00	45.79
ATOM	94	CB	SER	A	14	-5.005	23.386	58.825	1.00	34.33
ATOM	95	OG	SER	A	14	-6.006	23.978	59.621	1.00	41.01
ATOM	96	N	VAL	A	15	-6.785	25.327	56.630	1.00	32.80
ATOM	97	CA	VAL	A	15	-8.036	25.529	55.917	1.00	31.81

ATOM	98	C	VAL	A	15	-7.777	26.107	54.507	1.00	34.70
ATOM	99	O	VAL	A	15	-8.241	25.576	53.494	1.00	31.96
ATOM	100	CB	VAL	A	15	-9.033	26.336	56.720	1.00	33.07
ATOM	101	CG1	VAL	A	15	-10.272	26.638	55.861	1.00	33.31
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ATOM	103	N	CYS	A	16	-6.990	27.183	54.453	1.00	33.85
ATOM	104	CA	CYS	A	16	-6.602	27.826	53.189	1.00	38.27
ATOM	105	C	CYS	A	16	-5.206	28.388	53.265	1.00	37.14
ATOM	106	O	CYS	A	16	-4.616	28.534	54.322	1.00	39.70
ATOM	107	CB	CYS	A	16	-7.589	28.870	52.581	1.00	42.09
ATOM	108	SG	CYS	A	16	-7.844	30.418	53.540	1.00	47.38
ATOM	109	N	ARG	A	17	-4.679	28.722	52.132	1.00	32.10
ATOM	110	CA	ARG	A	17	-3.349	29.262	52.101	1.00	32.54
ATOM	111	C	ARG	A	17	-3.210	30.307	51.005	1.00	34.56
ATOM	112	O	ARG	A	17	-3.511	30.065	49.842	1.00	35.07
ATOM	113	CB	ARG	A	17	-2.371	28.152	51.758	1.00	36.83
ATOM	114	CG	ARG	A	17	-1.779	27.391	52.915	1.00	40.61
ATOM	115	CD	ARG	A	17	-1.472	25.970	52.503	1.00	27.18
ATOM	116	NE	ARG	A	17	-1.963	25.026	53.501	1.00	52.41
ATOM	117	CZ	ARG	A	17	-1.244	24.036	54.035	1.00	69.41
ATOM	118	NH1	ARG	A	17	0.020	23.812	53.683	1.00	54.86
ATOM	119	NH2	ARG	A	17	-1.810	23.246	54.952	1.00	49.68
ATOM	120	N	THR	A	18	-2.711	31.454	51.378	1.00	27.06
ATOM	121	CA	THR	A	18	-2.489	32.477	50.428	1.00	26.12
ATOM	122	C	THR	A	18	-1.250	32.110	49.653	1.00	30.83
ATOM	123	O	THR	A	18	-0.174	31.964	50.194	1.00	29.06
ATOM	124	CB	THR	A	18	-2.276	33.810	51.134	1.00	34.27
ATOM	125	OG1	THR	A	18	-3.481	34.261	51.738	1.00	32.95
ATOM	126	CG2	THR	A	18	-1.730	34.839	50.156	1.00	35.91
ATOM	127	N	LYS	A	19	-1.408	31.955	48.365	1.00	31.55
ATOM	128	CA	LYS	A	19	-0.298	31.615	47.511	1.00	31.74
ATOM	129	C	LYS	A	19	0.359	32.848	46.906	1.00	33.90
ATOM	130	O	LYS	A	19	1.513	32.834	46.520	1.00	34.57
ATOM	131	CB	LYS	A	19	-0.795	30.697	46.398	1.00	36.08
ATOM	132	CG	LYS	A	19	-1.332	29.368	46.924	1.00	62.54
ATOM	133	CD	LYS	A	19	-0.281	28.257	47.057	1.00	82.23
ATOM	134	CE	LYS	A	19	0.093	27.880	48.496	1.00	77.50
ATOM	135	NZ	LYS	A	19	1.553	27.849	48.745	1.00	55.63
ATOM	136	N	HIS	A	20	-0.387	33.928	46.810	1.00	31.40
ATOM	137	CA	HIS	A	20	0.160	35.122	46.198	1.00	29.22
ATOM	138	C	HIS	A	20	-0.655	36.345	46.517	1.00	34.68
ATOM	139	O	HIS	A	20	-1.833	36.239	46.846	1.00	35.34
ATOM	140	CB	HIS	A	20	0.123	34.956	44.666	1.00	26.47
ATOM	141	CG	HIS	A	20	0.865	36.022	43.970	1.00	26.77
ATOM	142	ND1	HIS	A	20	2.249	36.046	43.980	1.00	28.92
ATOM	143	CD2	HIS	A	20	0.415	37.091	43.280	1.00	27.43
ATOM	144	CE1	HIS	A	20	2.622	37.126	43.301	1.00	28.21
ATOM	145	NE2	HIS	A	20	1.536	37.781	42.865	1.00	28.18
ATOM	146	N	LEU	A	21	0.000	37.492	46.390	1.00	30.14
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ATOM	149	O	LEU	A	21	1.073	39.952	45.312	1.00	37.30
ATOM	150	CB	LEU	A	21	-0.342	39.363	47.999	1.00	31.30
ATOM	151	CG	LEU	A	21	-0.611	40.880	48.047	1.00	32.33
ATOM	152	CD1	LEU	A	21	-2.088	41.192	48.324	1.00	27.10
ATOM	153	CD2	LEU	A	21	0.277	41.522	49.100	1.00	32.86
ATOM	154	N	HIS	A	22	-1.127	40.442	44.951	1.00	35.47
ATOM	155	CA	HIS	A	22	-0.895	41.452	43.920	1.00	34.24
ATOM	156	C	HIS	A	22	-1.249	42.742	44.550	1.00	33.99
ATOM	157	O	HIS	A	22	-2.402	42.957	44.905	1.00	35.72
ATOM	158	CB	HIS	A	22	-1.720	41.244	42.624	1.00	33.38
ATOM	159	CG	HIS	A	22	-1.350	42.256	41.615	1.00	35.97
ATOM	160	ND1	HIS	A	22	-0.030	42.576	41.384	1.00	38.81
ATOM	161	CD2	HIS	A	22	-2.125	43.043	40.830	1.00	39.07

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ATOM    162  CE1 HIS A  22      -0.019  43.534  40.462  1.00 38.66
ATOM    163  NE2 HIS A  22      -1.262  43.829  40.103  1.00 39.13
ATOM    164  N   LEU A  23      -0.235  43.539  44.757  1.00 30.17
ATOM    165  CA  LEU A  23      -0.416  44.793  45.405  1.00 33.32
ATOM    166  C   LEU A  23      -0.203  45.949  44.440  1.00 44.46
ATOM    167  O   LEU A  23       0.828  46.068  43.761  1.00 44.06
ATOM    168  CB  LEU A  23       0.446  44.882  46.680  1.00 33.72
ATOM    169  CG  LEU A  23      -0.141  45.682  47.871  1.00 33.15
ATOM    170  CD1 LEU A  23       0.780  46.835  48.172  1.00 26.07
ATOM    171  CD2 LEU A  23      -1.539  46.213  47.609  1.00 35.39
ATOM    172  N   ARG A  24      -1.256  46.765  44.395  1.00 42.83
ATOM    173  CA  ARG A  24      -1.406  47.964  43.596  1.00 41.79
ATOM    174  C   ARG A  24      -1.930  49.005  44.562  1.00 39.15
ATOM    175  O   ARG A  24      -3.025  48.859  45.107  1.00 39.85
ATOM    176  CB  ARG A  24      -2.458  47.716  42.504  1.00 46.35
ATOM    177  CG  ARG A  24      -2.054  46.750  41.382  1.00 50.50
ATOM    178  CD  ARG A  24      -2.754  47.058  40.043  1.00 80.27
ATOM    179  NE  ARG A  24      -4.200  46.798  40.062  1.00 95.12
ATOM    180  CZ  ARG A  24      -5.152  47.703  39.826  1.00100.00
ATOM    181  NH1 ARG A  24      -4.863  48.973  39.483  1.00100.00
ATOM    182  NH2 ARG A  24      -6.432  47.326  39.865  1.00100.00
ATOM    183  N   CYS A  25      -1.164  50.028  44.844  1.00 32.39
ATOM    184  CA  CYS A  25      -1.698  50.969  45.813  1.00 33.30
ATOM    185  C   CYS A  25      -1.061  52.325  45.724  1.00 34.82
ATOM    186  O   CYS A  25      -0.012  52.514  45.076  1.00 31.03
ATOM    187  CB  CYS A  25      -1.503  50.440  47.257  1.00 34.67
ATOM    188  SG  CYS A  25       0.231  50.529  47.798  1.00 38.07
ATOM    189  N   SER A  26      -1.711  53.257  46.418  1.00 34.39
ATOM    190  CA  SER A  26      -1.196  54.601  46.437  1.00 36.77
ATOM    191  C   SER A  26      -0.963  55.133  47.821  1.00 39.85
ATOM    192  O   SER A  26      -1.738  54.853  48.757  1.00 37.56
ATOM    193  CB  SER A  26      -1.889  55.600  45.530  1.00 42.70
ATOM    194  OG  SER A  26      -0.899  56.330  44.824  1.00 61.74
ATOM    195  N   VAL A  27       0.133  55.897  47.886  1.00 39.43
ATOM    196  CA  VAL A  27       0.624  56.583  49.081  1.00 41.31
ATOM    197  C   VAL A  27       0.209  58.043  49.082  1.00 44.32
ATOM    198  O   VAL A  27       0.562  58.799  48.187  1.00 45.24
ATOM    199  CB  VAL A  27       2.135  56.531  49.207  1.00 46.35
ATOM    200  CG1 VAL A  27       2.524  57.207  50.522  1.00 45.62
ATOM    201  CG2 VAL A  27       2.592  55.079  49.178  1.00 47.20
ATOM    202  N   ASP A  28      -0.553  58.417  50.093  1.00 37.94
ATOM    203  CA  ASP A  28      -1.040  59.764  50.237  1.00 35.28
ATOM    204  C   ASP A  28      -0.595  60.366  51.538  1.00 33.85
ATOM    205  O   ASP A  28      -1.181  60.099  52.598  1.00 28.52
ATOM    206  CB  ASP A  28      -2.559  59.807  50.189  1.00 37.09
ATOM    207  CG  ASP A  28      -3.055  61.205  50.095  1.00 55.20
ATOM    208  OD1 ASP A  28      -2.611  62.119  50.767  1.00 59.17
ATOM    209  OD2 ASP A  28      -3.993  61.335  49.192  1.00 61.41
ATOM    210  N   PHE A  29       0.436  61.174  51.405  1.00 36.42
ATOM    211  CA  PHE A  29       1.044  61.888  52.512  1.00 43.07
ATOM    212  C   PHE A  29       0.105  62.928  53.077  1.00 51.14
ATOM    213  O   PHE A  29       0.161  63.279  54.257  1.00 51.35
ATOM    214  CB  PHE A  29       2.410  62.517  52.143  1.00 47.77
ATOM    215  CG  PHE A  29       3.519  61.485  52.079  1.00 50.86
ATOM    216  CD1 PHE A  29       4.066  60.957  53.247  1.00 52.08
ATOM    217  CD2 PHE A  29       3.996  61.001  50.863  1.00 53.94
ATOM    218  CE1 PHE A  29       5.075  59.995  53.215  1.00 52.83
ATOM    219  CE2 PHE A  29       5.013  60.046  50.813  1.00 56.46
ATOM    220  CZ  PHE A  29       5.559  59.538  51.992  1.00 53.39
ATOM    221  N   THR A  30      -0.766  63.420  52.220  1.00 47.10
ATOM    222  CA  THR A  30      -1.718  64.386  52.654  1.00 45.48
ATOM    223  C   THR A  30      -2.788  63.715  53.509  1.00 48.41
ATOM    224  O   THR A  30      -3.045  64.082  54.649  1.00 48.64
ATOM    225  CB  THR A  30      -2.283  65.097  51.434  1.00 54.06
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ATOM	226	OG1	THR	A	30	-1.428	66.186	51.107	1.00 50.68
ATOM	227	CG2	THR	A	30	-3.697	65.568	51.745	1.00 60.28
ATOM	228	N	ARG	A	31	-3.392	62.683	52.978	1.00 46.66
ATOM	229	CA	ARG	A	31	-4.404	61.987	53.734	1.00 47.88
ATOM	230	C	ARG	A	31	-3.826	60.999	54.750	1.00 45.46
ATOM	231	O	ARG	A	31	-4.590	60.468	55.551	1.00 41.52
ATOM	232	CB	ARG	A	31	-5.335	61.214	52.805	1.00 56.73
ATOM	233	CG	ARG	A	31	-5.950	62.065	51.700	1.00 84.16
ATOM	234	CD	ARG	A	31	-7.338	61.568	51.284	1.00100.00
ATOM	235	NE	ARG	A	31	-7.344	60.450	50.327	1.00100.00
ATOM	236	CZ	ARG	A	31	-8.148	60.371	49.251	1.00100.00
ATOM	237	NH1	ARG	A	31	-9.034	61.324	48.944	1.00100.00
ATOM	238	NH2	ARG	A	31	-8.062	59.298	48.460	1.00100.00
ATOM	239	N	ARG	A	32	-2.489	60.752	54.683	1.00 39.71
ATOM	240	CA	ARG	A	32	-1.751	59.798	55.531	1.00 39.09
ATOM	241	C	ARG	A	32	-2.324	58.411	55.379	1.00 39.62
ATOM	242	O	ARG	A	32	-2.495	57.655	56.337	1.00 33.10
ATOM	243	CB	ARG	A	32	-1.523	60.115	57.022	1.00 37.14
ATOM	244	CG	ARG	A	32	-1.197	61.569	57.337	1.00 71.25
ATOM	245	CD	ARG	A	32	0.277	61.834	57.686	1.00100.00
ATOM	246	NE	ARG	A	32	0.703	61.299	58.986	1.00100.00
ATOM	247	CZ	ARG	A	32	1.284	62.005	59.961	1.00 79.51
ATOM	248	NH1	ARG	A	32	1.522	63.308	59.831	1.00 55.73
ATOM	249	NH2	ARG	A	32	1.626	61.387	61.098	1.00 44.96
ATOM	250	N	THR	A	33	-2.612	58.068	54.139	1.00 39.83
ATOM	251	CA	THR	A	33	-3.162	56.752	53.902	1.00 39.31
ATOM	252	C	THR	A	33	-2.543	56.010	52.760	1.00 41.13
ATOM	253	O	THR	A	33	-1.853	56.574	51.926	1.00 42.93
ATOM	254	CB	THR	A	33	-4.635	56.835	53.641	1.00 43.44
ATOM	255	OG1	THR	A	33	-4.798	57.636	52.468	1.00 40.17
ATOM	256	CG2	THR	A	33	-5.245	57.468	54.880	1.00 38.71
ATOM	257	N	LEU	A	34	-2.822	54.717	52.762	1.00 35.26
ATOM	258	CA	LEU	A	34	-2.372	53.799	51.745	1.00 35.20
ATOM	259	C	LEU	A	34	-3.632	53.293	51.098	1.00 32.49
ATOM	260	O	LEU	A	34	-4.474	52.670	51.751	1.00 30.96
ATOM	261	CB	LEU	A	34	-1.522	52.651	52.322	1.00 37.07
ATOM	262	CG	LEU	A	34	-0.149	52.571	51.685	1.00 42.99
ATOM	263	CD1	LEU	A	34	0.648	51.425	52.285	1.00 40.58
ATOM	264	CD2	LEU	A	34	-0.360	52.302	50.208	1.00 50.83
ATOM	265	N	THR	A	35	-3.800	53.632	49.838	1.00 28.72
ATOM	266	CA	THR	A	35	-5.017	53.228	49.198	1.00 31.26
ATOM	267	C	THR	A	35	-4.838	52.329	48.013	1.00 36.54
ATOM	268	O	THR	A	35	-3.940	52.546	47.187	1.00 34.70
ATOM	269	CB	THR	A	35	-5.877	54.427	48.813	1.00 44.88
ATOM	270	OG1	THR	A	35	-5.484	55.549	49.579	1.00 58.59
ATOM	271	CG2	THR	A	35	-7.324	54.094	49.109	1.00 49.42
ATOM	272	N	GLY	A	36	-5.726	51.329	47.950	1.00 32.57
ATOM	273	CA	GLY	A	36	-5.696	50.405	46.837	1.00 33.89
ATOM	274	C	GLY	A	36	-6.418	49.074	46.993	1.00 34.50
ATOM	275	O	GLY	A	36	-7.441	48.919	47.678	1.00 31.78
ATOM	276	N	THR	A	37	-5.836	48.103	46.293	1.00 35.93
ATOM	277	CA	THR	A	37	-6.327	46.723	46.281	1.00 36.12
ATOM	278	C	THR	A	37	-5.268	45.696	46.473	1.00 35.67
ATOM	279	O	THR	A	37	-4.155	45.795	45.964	1.00 33.86
ATOM	280	CB	THR	A	37	-7.119	46.306	45.050	1.00 42.21
ATOM	281	OG1	THR	A	37	-6.507	46.804	43.870	1.00 30.98
ATOM	282	CG2	THR	A	37	-8.547	46.793	45.229	1.00 50.03
ATOM	283	N	ALA	A	38	-5.687	44.705	47.220	1.00 32.95
ATOM	284	CA	ALA	A	38	-4.886	43.570	47.533	1.00 33.45
ATOM	285	C	ALA	A	38	-5.481	42.374	46.824	1.00 35.47
ATOM	286	O	ALA	A	38	-6.580	41.906	47.151	1.00 32.91
ATOM	287	CB	ALA	A	38	-4.845	43.341	49.044	1.00 33.72
ATOM	288	N	ALA	A	39	-4.764	41.874	45.834	1.00 32.70
ATOM	289	CA	ALA	A	39	-5.274	40.702	45.140	1.00 31.59

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ATOM    290  C   ALA A  39      -4.692  39.464  45.770  1.00 32.11
ATOM    291  O   ALA A  39      -3.514  39.147  45.608  1.00 32.46
ATOM    292  CB  ALA A  39      -4.934  40.729  43.662  1.00 32.13
ATOM    293  N   LEU A  40      -5.505  38.774  46.508  1.00 27.06
ATOM    294  CA  LEU A  40      -5.001  37.593  47.155  1.00 29.04
ATOM    295  C   LEU A  40      -5.331  36.322  46.364  1.00 36.88
ATOM    296  O   LEU A  40      -6.485  36.100  45.963  1.00 28.89
ATOM    297  CB  LEU A  40      -5.587  37.451  48.600  1.00 29.39
ATOM    298  CG  LEU A  40      -5.303  38.598  49.559  1.00 31.39
ATOM    299  CD1 LEU A  40      -5.435  38.063  50.970  1.00 32.62
ATOM    300  CD2 LEU A  40      -3.879  39.019  49.355  1.00 31.60
ATOM    301  N   THR A  41      -4.310  35.470  46.165  1.00 42.40
ATOM    302  CA  THR A  41      -4.523  34.210  45.488  1.00 43.93
ATOM    303  C   THR A  41      -4.548  33.155  46.552  1.00 43.75
ATOM    304  O   THR A  41      -3.510  32.827  47.115  1.00 45.22
ATOM    305  CB  THR A  41      -3.511  33.892  44.402  1.00 55.44
ATOM    306  OG1 THR A  41      -3.604  34.885  43.418  1.00 55.57
ATOM    307  CG2 THR A  41      -3.872  32.544  43.802  1.00 47.78
ATOM    308  N   VAL A  42      -5.755  32.688  46.848  1.00 33.25
ATOM    309  CA  VAL A  42      -5.946  31.720  47.893  1.00 32.21
ATOM    310  C   VAL A  42      -6.166  30.312  47.380  1.00 40.56
ATOM    311  O   VAL A  42      -6.827  30.105  46.376  1.00 42.56
ATOM    312  CB  VAL A  42      -7.017  32.153  48.920  1.00 36.45
ATOM    313  CG1 VAL A  42      -6.817  31.451  50.266  1.00 36.89
ATOM    314  CG2 VAL A  42      -6.963  33.665  49.170  1.00 36.10
ATOM    315  N   GLN A  43      -5.590  29.357  48.117  1.00 35.91
ATOM    316  CA  GLN A  43      -5.678  27.945  47.838  1.00 31.59
ATOM    317  C   GLN A  43      -6.346  27.244  48.988  1.00 38.98
ATOM    318  O   GLN A  43      -5.916  27.317  50.144  1.00 40.92
ATOM    319  CB  GLN A  43      -4.305  27.319  47.568  1.00 30.50
ATOM    320  CG  GLN A  43      -4.362  25.800  47.259  1.00 53.80
ATOM    321  CD  GLN A  43      -2.986  25.177  47.099  1.00 62.47
ATOM    322  OE1 GLN A  43      -2.569  24.842  45.978  1.00 57.34
ATOM    323  NE2 GLN A  43      -2.274  25.037  48.224  1.00 43.72
ATOM    324  N   SER A  44      -7.423  26.555  48.664  1.00 33.83
ATOM    325  CA  SER A  44      -8.166  25.839  49.678  1.00 31.38
ATOM    326  C   SER A  44      -7.495  24.557  50.117  1.00 42.10
ATOM    327  O   SER A  44      -6.955  23.814  49.292  1.00 42.78
ATOM    328  CB  SER A  44      -9.576  25.530  49.226  1.00 28.60
ATOM    329  OG  SER A  44     -10.234  24.785  50.224  1.00 34.57
ATOM    330  N   GLN A  45      -7.579  24.286  51.423  1.00 38.84
ATOM    331  CA  GLN A  45      -7.007  23.082  51.994  1.00 37.05
ATOM    332  C   GLN A  45      -8.082  22.050  52.269  1.00 47.57
ATOM    333  O   GLN A  45      -7.801  20.917  52.678  1.00 42.94
ATOM    334  CB  GLN A  45      -6.247  23.411  53.280  1.00 36.10
ATOM    335  CG  GLN A  45      -5.246  24.539  53.034  1.00 54.73
ATOM    336  CD  GLN A  45      -4.323  24.206  51.888  1.00 45.43
ATOM    337  OE1 GLN A  45      -4.257  24.888  50.833  1.00 39.23
ATOM    338  NE2 GLN A  45      -3.621  23.121  52.092  1.00 29.80
ATOM    339  N   GLU A  46      -9.330  22.459  52.048  1.00 50.54
ATOM    340  CA  GLU A  46     -10.454  21.573  52.283  1.00 50.99
ATOM    341  C   GLU A  46     -11.496  21.583  51.179  1.00 54.49
ATOM    342  O   GLU A  46     -11.518  22.406  50.261  1.00 54.00
ATOM    343  CB  GLU A  46     -11.139  21.793  53.657  1.00 51.61
ATOM    344  CG  GLU A  46     -10.581  22.979  54.454  1.00 55.93
ATOM    345  CD  GLU A  46     -11.427  23.329  55.646  1.00 78.67
ATOM    346  OE1 GLU A  46     -12.563  23.765  55.543  1.00 69.56
ATOM    347  OE2 GLU A  46     -10.814  23.129  56.796  1.00 75.10
ATOM    348  N   ASP A  47     -12.387  20.630  51.300  1.00 48.90
ATOM    349  CA  ASP A  47     -13.450  20.549  50.362  1.00 49.03
ATOM    350  C   ASP A  47     -14.591  21.425  50.846  1.00 55.15
ATOM    351  O   ASP A  47     -14.760  21.631  52.044  1.00 56.66
ATOM    352  CB  ASP A  47     -13.913  19.099  50.227  1.00 50.20
ATOM    353  CG  ASP A  47     -13.083  18.376  49.218  1.00 66.88
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ATOM    354  OD1 ASP A  47     -12.340  18.945  48.434  1.00 66.27
ATOM    355  OD2 ASP A  47     -13.235  17.081  49.284  1.00 76.37
ATOM    356  N   ASN A  48     -15.391  21.941  49.929  1.00 50.25
ATOM    357  CA  ASN A  48     -16.519  22.755  50.339  1.00 48.45
ATOM    358  C   ASN A  48     -16.115  24.000  51.115  1.00 43.07
ATOM    359  O   ASN A  48     -16.699  24.351  52.138  1.00 39.78
ATOM    360  CB  ASN A  48     -17.559  21.909  51.117  1.00 51.19
ATOM    361  CG  ASN A  48     -18.985  22.417  51.005  1.00 76.39
ATOM    362  OD1 ASN A  48     -19.594  22.348  49.929  1.00 85.15
ATOM    363  ND2 ASN A  48     -19.515  22.928  52.115  1.00 68.29
ATOM    364  N   LEU A  49     -15.113  24.688  50.628  1.00 35.36
ATOM    365  CA  LEU A  49     -14.728  25.874  51.335  1.00 34.40
ATOM    366  C   LEU A  49     -15.601  27.009  50.851  1.00 47.38
ATOM    367  O   LEU A  49     -15.421  27.515  49.734  1.00 45.47
ATOM    368  CB  LEU A  49     -13.239  26.152  51.173  1.00 31.04
ATOM    369  CG  LEU A  49     -12.781  27.394  51.885  1.00 29.82
ATOM    370  CD1 LEU A  49     -12.725  27.137  53.385  1.00 28.15
ATOM    371  CD2 LEU A  49     -11.394  27.753  51.368  1.00 30.24
ATOM    372  N   ARG A  50     -16.568  27.363  51.699  1.00 50.49
ATOM    373  CA  ARG A  50     -17.560  28.392  51.401  1.00 52.83
ATOM    374  C   ARG A  50     -17.169  29.838  51.702  1.00 55.57
ATOM    375  O   ARG A  50     -17.627  30.760  51.011  1.00 53.89
ATOM    376  CB  ARG A  50     -18.928  28.028  51.986  1.00 58.35
ATOM    377  CG  ARG A  50     -19.863  27.354  50.980  1.00 74.76
ATOM    378  CD  ARG A  50     -20.438  26.024  51.462  1.00 81.60
ATOM    379  NE  ARG A  50     -21.214  25.355  50.415  1.00 94.37
ATOM    380  CZ  ARG A  50     -22.465  24.888  50.538  1.00100.00
ATOM    381  NH1 ARG A  50     -23.151  24.990  51.687  1.00100.00
ATOM    382  NH2 ARG A  50     -23.046  24.297  49.471  1.00 74.34
ATOM    383  N   SER A  51     -16.331  30.006  52.743  1.00 54.71
ATOM    384  CA  SER A  51     -15.823  31.297  53.224  1.00 53.49
ATOM    385  C   SER A  51     -14.495  31.156  53.955  1.00 53.57
ATOM    386  O   SER A  51     -14.146  30.062  54.420  1.00 52.93
ATOM    387  CB  SER A  51     -16.788  31.900  54.232  1.00 54.03
ATOM    388  OG  SER A  51     -16.871  31.048  55.373  1.00 45.15
ATOM    389  N   LEU A  52     -13.796  32.298  54.067  1.00 47.19
ATOM    390  CA  LEU A  52     -12.519  32.422  54.762  1.00 45.66
ATOM    391  C   LEU A  52     -12.415  33.671  55.640  1.00 50.43
ATOM    392  O   LEU A  52     -13.145  34.633  55.471  1.00 52.64
ATOM    393  CB  LEU A  52     -11.235  32.117  53.923  1.00 44.20
ATOM    394  CG  LEU A  52     -10.896  33.044  52.745  1.00 43.98
ATOM    395  CD1 LEU A  52     -11.739  32.687  51.554  1.00 42.82
ATOM    396  CD2 LEU A  52     -11.128  34.501  53.094  1.00 44.71
ATOM    397  N   VAL A  53     -11.483  33.658  56.579  1.00 44.97
ATOM    398  CA  VAL A  53     -11.271  34.781  57.455  1.00 41.69
ATOM    399  C   VAL A  53      -9.859  35.309  57.339  1.00 44.25
ATOM    400  O   VAL A  53      -8.866  34.551  57.302  1.00 45.42
ATOM    401  CB  VAL A  53     -11.565  34.420  58.906  1.00 45.48
ATOM    402  CG1 VAL A  53     -11.223  35.554  59.853  1.00 44.94
ATOM    403  CG2 VAL A  53     -13.030  34.073  59.050  1.00 45.79
ATOM    404  N   LEU A  54      -9.796  36.627  57.166  1.00 35.12
ATOM    405  CA  LEU A  54      -8.555  37.333  57.080  1.00 34.14
ATOM    406  C   LEU A  54      -8.377  38.207  58.326  1.00 38.92
ATOM    407  O   LEU A  54      -9.281  38.457  59.108  1.00 37.45
ATOM    408  CB  LEU A  54      -8.461  38.216  55.831  1.00 34.73
ATOM    409  CG  LEU A  54      -8.539  37.469  54.510  1.00 40.25
ATOM    410  CD1 LEU A  54      -8.416  38.488  53.374  1.00 40.69
ATOM    411  CD2 LEU A  54      -7.424  36.428  54.415  1.00 39.64
ATOM    412  N   ASP A  55      -7.192  38.674  58.524  1.00 35.02
ATOM    413  CA  ASP A  55      -6.918  39.526  59.627  1.00 31.65
ATOM    414  C   ASP A  55      -6.956  40.941  59.078  1.00 40.38
ATOM    415  O   ASP A  55      -6.754  41.151  57.886  1.00 39.98
ATOM    416  CB  ASP A  55      -5.494  39.232  60.075  1.00 30.92
ATOM    417  CG  ASP A  55      -5.397  38.103  61.037  1.00 35.96
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ATOM	418	OD1	ASP	A	55	-6.049	38.074	62.066	1.00	38.49
ATOM	419	OD2	ASP	A	55	-4.491	37.205	60.682	1.00	36.53
ATOM	420	N	THR	A	56	-7.196	41.900	59.963	1.00	42.93
ATOM	421	CA	THR	A	56	-7.243	43.334	59.661	1.00	41.75
ATOM	422	C	THR	A	56	-7.101	44.128	60.967	1.00	37.46
ATOM	423	O	THR	A	56	-7.517	43.687	62.049	1.00	36.98
ATOM	424	CB	THR	A	56	-8.514	43.825	58.894	1.00	37.17
ATOM	425	OG1	THR	A	56	-9.587	43.957	59.805	1.00	31.84
ATOM	426	CG2	THR	A	56	-8.910	42.943	57.714	1.00	33.58
ATOM	427	N	LYS	A	57	-6.513	45.304	60.863	1.00	26.63
ATOM	428	CA	LYS	A	57	-6.363	46.134	62.020	1.00	25.64
ATOM	429	C	LYS	A	57	-6.585	47.539	61.547	1.00	30.08
ATOM	430	O	LYS	A	57	-5.854	48.012	60.711	1.00	25.68
ATOM	431	CB	LYS	A	57	-4.991	45.983	62.641	1.00	27.34
ATOM	432	CG	LYS	A	57	-4.907	46.387	64.100	1.00	35.83
ATOM	433	CD	LYS	A	57	-3.514	46.904	64.471	1.00	35.57
ATOM	434	CE	LYS	A	57	-2.901	46.225	65.689	1.00	50.54
ATOM	435	NZ	LYS	A	57	-2.521	47.180	66.757	1.00	55.43
ATOM	436	N	ASP	A	58	-7.617	48.188	62.065	1.00	32.68
ATOM	437	CA	ASP	A	58	-7.895	49.545	61.665	1.00	35.27
ATOM	438	C	ASP	A	58	-7.894	49.710	60.149	1.00	38.24
ATOM	439	O	ASP	A	58	-7.289	50.627	59.571	1.00	35.86
ATOM	440	CB	ASP	A	58	-6.968	50.550	62.386	1.00	37.22
ATOM	441	CG	ASP	A	58	-7.041	50.393	63.880	1.00	50.71
ATOM	442	OD1	ASP	A	58	-8.073	50.136	64.478	1.00	57.20
ATOM	443	OD2	ASP	A	58	-5.878	50.562	64.463	1.00	45.82
ATOM	444	N	LEU	A	59	-8.604	48.796	59.516	1.00	37.68
ATOM	445	CA	LEU	A	59	-8.720	48.813	58.079	1.00	39.36
ATOM	446	C	LEU	A	59	-10.077	49.243	57.555	1.00	45.51
ATOM	447	O	LEU	A	59	-11.146	48.946	58.120	1.00	44.18
ATOM	448	CB	LEU	A	59	-8.265	47.506	57.422	1.00	38.42
ATOM	449	CG	LEU	A	59	-6.762	47.475	57.218	1.00	37.40
ATOM	450	CD1	LEU	A	59	-6.392	46.173	56.526	1.00	36.39
ATOM	451	CD2	LEU	A	59	-6.321	48.655	56.361	1.00	36.57
ATOM	452	N	THR	A	60	-9.984	49.949	56.437	1.00	42.59
ATOM	453	CA	THR	A	60	-11.132	50.483	55.734	1.00	42.63
ATOM	454	C	THR	A	60	-11.357	49.705	54.463	1.00	38.18
ATOM	455	O	THR	A	60	-10.632	49.856	53.454	1.00	34.33
ATOM	456	CB	THR	A	60	-11.030	52.028	55.532	1.00	65.15
ATOM	457	OG1	THR	A	60	-11.806	52.736	56.504	1.00	67.56
ATOM	458	CG2	THR	A	60	-11.345	52.480	54.104	1.00	56.89
ATOM	459	N	ILE	A	61	-12.360	48.847	54.571	1.00	33.39
ATOM	460	CA	ILE	A	61	-12.753	47.975	53.482	1.00	35.89
ATOM	461	C	ILE	A	61	-13.726	48.634	52.533	1.00	41.05
ATOM	462	O	ILE	A	61	-14.913	48.706	52.840	1.00	40.08
ATOM	463	CB	ILE	A	61	-13.403	46.670	53.944	1.00	39.71
ATOM	464	CG1	ILE	A	61	-12.482	45.826	54.832	1.00	39.90
ATOM	465	CG2	ILE	A	61	-13.788	45.900	52.691	1.00	38.96
ATOM	466	CD1	ILE	A	61	-11.027	45.851	54.358	1.00	49.61
ATOM	467	N	GLU	A	62	-13.219	49.080	51.391	1.00	40.23
ATOM	468	CA	GLU	A	62	-14.040	49.700	50.365	1.00	41.73
ATOM	469	C	GLU	A	62	-14.986	48.633	49.826	1.00	47.09
ATOM	470	O	GLU	A	62	-16.207	48.726	49.926	1.00	47.52
ATOM	471	CB	GLU	A	62	-13.138	50.272	49.239	1.00	44.08
ATOM	472	CG	GLU	A	62	-13.765	51.406	48.381	1.00	64.08
ATOM	473	CD	GLU	A	62	-14.686	50.946	47.256	1.00	100.00
ATOM	474	OE1	GLU	A	62	-15.458	50.002	47.376	1.00	100.00
ATOM	475	OE2	GLU	A	62	-14.591	51.670	46.146	1.00	75.11
ATOM	476	N	LYS	A	63	-14.399	47.580	49.267	1.00	43.46
ATOM	477	CA	LYS	A	63	-15.168	46.474	48.746	1.00	40.53
ATOM	478	C	LYS	A	63	-14.250	45.307	48.489	1.00	45.38
ATOM	479	O	LYS	A	63	-13.046	45.500	48.362	1.00	43.51
ATOM	480	CB	LYS	A	63	-15.818	46.830	47.428	1.00	40.46
ATOM	481	CG	LYS	A	63	-14.789	46.959	46.321	1.00	20.53

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ATOM    482  CD  LYS A  63     -15.367  47.555  45.054  1.00 28.36
ATOM    483  CE  LYS A  63     -14.315  48.158  44.139  1.00 40.61
ATOM    484  NZ  LYS A  63     -14.588  47.938  42.711  1.00 54.71
ATOM    485  N   VAL A  64     -14.862  44.116  48.441  1.00 45.57
ATOM    486  CA  VAL A  64     -14.190  42.844  48.171  1.00 44.90
ATOM    487  C   VAL A  64     -14.666  42.263  46.841  1.00 46.44
ATOM    488  O   VAL A  64     -15.826  41.917  46.700  1.00 45.81
ATOM    489  CB  VAL A  64     -14.505  41.748  49.192  1.00 46.24
ATOM    490  CG1 VAL A  64     -13.864  40.471  48.669  1.00 44.81
ATOM    491  CG2 VAL A  64     -14.040  42.048  50.627  1.00 44.77
ATOM    492  N   VAL A  65     -13.793  42.099  45.875  1.00 43.10
ATOM    493  CA  VAL A  65     -14.240  41.537  44.604  1.00 41.42
ATOM    494  C   VAL A  65     -13.707  40.156  44.282  1.00 42.13
ATOM    495  O   VAL A  65     -12.605  39.787  44.660  1.00 42.64
ATOM    496  CB  VAL A  65     -13.856  42.462  43.484  1.00 44.58
ATOM    497  CG1 VAL A  65     -14.520  42.037  42.189  1.00 42.79
ATOM    498  CG2 VAL A  65     -14.264  43.874  43.883  1.00 45.05
ATOM    499  N   ILE A  66     -14.515  39.402  43.556  1.00 38.68
ATOM    500  CA  ILE A  66     -14.179  38.053  43.113  1.00 39.98
ATOM    501  C   ILE A  66     -14.899  37.774  41.802  1.00 44.86
ATOM    502  O   ILE A  66     -16.136  37.735  41.729  1.00 42.69
ATOM    503  CB  ILE A  66     -14.520  36.947  44.113  1.00 44.28
ATOM    504  CG1 ILE A  66     -13.813  37.127  45.445  1.00 47.27
ATOM    505  CG2 ILE A  66     -14.141  35.578  43.550  1.00 42.84
ATOM    506  CD1 ILE A  66     -14.352  36.169  46.514  1.00 38.79
ATOM    507  N   ASN A  67     -14.120  37.549  40.759  1.00 42.94
ATOM    508  CA  ASN A  67     -14.715  37.266  39.472  1.00 44.24
ATOM    509  C   ASN A  67     -15.541  38.444  39.008  1.00 54.25
ATOM    510  O   ASN A  67     -16.743  38.344  38.768  1.00 57.56
ATOM    511  CB  ASN A  67     -15.595  36.007  39.507  1.00 40.72
ATOM    512  CG  ASN A  67     -14.788  34.759  39.745  1.00 57.39
ATOM    513  OD1 ASN A  67     -13.581  34.711  39.454  1.00 52.63
ATOM    514  ND2 ASN A  67     -15.446  33.760  40.317  1.00 44.54
ATOM    515  N   GLY A  68     -14.876  39.574  38.899  1.00 50.43
ATOM    516  CA  GLY A  68     -15.517  40.796  38.462  1.00 48.89
ATOM    517  C   GLY A  68     -16.807  41.115  39.194  1.00 48.77
ATOM    518  O   GLY A  68     -17.523  42.018  38.803  1.00 51.39
ATOM    519  N   GLN A  69     -17.129  40.385  40.244  1.00 40.06
ATOM    520  CA  GLN A  69     -18.348  40.716  40.928  1.00 40.02
ATOM    521  C   GLN A  69     -18.031  41.059  42.364  1.00 50.45
ATOM    522  O   GLN A  69     -16.943  40.748  42.855  1.00 50.53
ATOM    523  CB  GLN A  69     -19.415  39.602  40.829  1.00 40.78
ATOM    524  CG  GLN A  69     -19.966  39.367  39.414  1.00 23.77
ATOM    525  CD  GLN A  69     -20.513  40.646  38.831  1.00 56.53
ATOM    526  OE1 GLN A  69     -19.974  41.198  37.859  1.00 55.28
ATOM    527  NE2 GLN A  69     -21.588  41.134  39.437  1.00 62.26
ATOM    528  N   GLU A  70     -18.975  41.718  43.028  1.00 49.43
ATOM    529  CA  GLU A  70     -18.766  42.094  44.407  1.00 50.67
ATOM    530  C   GLU A  70     -19.296  40.996  45.288  1.00 57.90
ATOM    531  O   GLU A  70     -20.272  40.367  44.909  1.00 63.90
ATOM    532  CB  GLU A  70     -19.449  43.434  44.732  1.00 52.26
ATOM    533  CG  GLU A  70     -18.824  44.624  43.970  1.00 64.80
ATOM    534  CD  GLU A  70     -19.181  45.967  44.555  1.00 91.82
ATOM    535  OE1 GLU A  70     -19.749  46.108  45.629  1.00100.00
ATOM    536  OE2 GLU A  70     -18.814  46.963  43.785  1.00 76.01
ATOM    537  N   VAL A  71     -18.655  40.742  46.433  1.00 47.28
ATOM    538  CA  VAL A  71     -19.119  39.685  47.335  1.00 43.84
ATOM    539  C   VAL A  71     -19.434  40.153  48.768  1.00 41.62
ATOM    540  O   VAL A  71     -18.983  41.206  49.254  1.00 35.70
ATOM    541  CB  VAL A  71     -18.308  38.361  47.273  1.00 46.05
ATOM    542  CG1 VAL A  71     -18.062  37.923  45.827  1.00 45.19
ATOM    543  CG2 VAL A  71     -16.979  38.460  48.017  1.00 45.24
ATOM    544  N   LYS A  72     -20.239  39.343  49.431  1.00 39.34
ATOM    545  CA  LYS A  72     -20.610  39.594  50.792  1.00 42.40
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ATOM	546	C	LYS	A	72	-19.347	39.466	51.668	1.00	56.92
ATOM	547	O	LYS	A	72	-18.399	38.729	51.334	1.00	59.27
ATOM	548	CB	LYS	A	72	-21.719	38.629	51.211	1.00	45.76
ATOM	549	CG	LYS	A	72	-22.378	38.960	52.557	1.00	86.98
ATOM	550	CD	LYS	A	72	-23.898	38.767	52.606	1.00	100.00
ATOM	551	CE	LYS	A	72	-24.656	40.012	53.077	1.00	100.00
ATOM	552	NZ	LYS	A	72	-26.011	39.730	53.592	1.00	100.00
ATOM	553	N	TYR	A	73	-19.332	40.210	52.780	1.00	55.45
ATOM	554	CA	TYR	A	73	-18.236	40.226	53.747	1.00	53.31
ATOM	555	C	TYR	A	73	-18.636	40.884	55.068	1.00	50.87
ATOM	556	O	TYR	A	73	-19.552	41.703	55.139	1.00	47.82
ATOM	557	CB	TYR	A	73	-16.891	40.741	53.214	1.00	52.73
ATOM	558	CG	TYR	A	73	-16.765	42.244	53.227	1.00	51.76
ATOM	559	CD1	TYR	A	73	-16.539	42.946	54.416	1.00	52.82
ATOM	560	CD2	TYR	A	73	-16.927	42.967	52.039	1.00	53.30
ATOM	561	CE1	TYR	A	73	-16.439	44.340	54.422	1.00	52.71
ATOM	562	CE2	TYR	A	73	-16.804	44.359	52.026	1.00	55.39
ATOM	563	CZ	TYR	A	73	-16.592	45.044	53.229	1.00	63.45
ATOM	564	OH	TYR	A	73	-16.471	46.404	53.215	1.00	69.53
ATOM	565	N	ALA	A	74	-17.927	40.494	56.112	1.00	45.37
ATOM	566	CA	ALA	A	74	-18.180	40.999	57.433	1.00	42.62
ATOM	567	C	ALA	A	74	-16.892	41.265	58.222	1.00	47.81
ATOM	568	O	ALA	A	74	-15.894	40.554	58.133	1.00	45.50
ATOM	569	CB	ALA	A	74	-19.111	40.035	58.170	1.00	40.75
ATOM	570	N	LEU	A	75	-16.930	42.323	59.005	1.00	49.02
ATOM	571	CA	LEU	A	75	-15.829	42.693	59.869	1.00	48.85
ATOM	572	C	LEU	A	75	-16.319	42.464	61.281	1.00	47.18
ATOM	573	O	LEU	A	75	-17.309	43.021	61.687	1.00	44.35
ATOM	574	CB	LEU	A	75	-15.332	44.136	59.675	1.00	49.64
ATOM	575	CG	LEU	A	75	-14.789	44.357	58.270	1.00	58.09
ATOM	576	CD1	LEU	A	75	-14.524	45.841	58.023	1.00	61.34
ATOM	577	CD2	LEU	A	75	-13.512	43.565	58.069	1.00	62.34
ATOM	578	N	GLY	A	76	-15.647	41.592	62.004	1.00	47.67
ATOM	579	CA	GLY	A	76	-16.034	41.281	63.359	1.00	46.79
ATOM	580	C	GLY	A	76	-15.495	42.337	64.279	1.00	47.74
ATOM	581	O	GLY	A	76	-14.656	43.171	63.882	1.00	42.87
ATOM	582	N	GLU	A	77	-15.988	42.311	65.502	1.00	48.32
ATOM	583	CA	GLU	A	77	-15.526	43.300	66.431	1.00	52.14
ATOM	584	C	GLU	A	77	-14.029	43.195	66.679	1.00	56.71
ATOM	585	O	GLU	A	77	-13.418	42.120	66.591	1.00	55.78
ATOM	586	CB	GLU	A	77	-16.357	43.341	67.732	1.00	55.55
ATOM	587	CG	GLU	A	77	-17.198	42.063	67.969	1.00	79.57
ATOM	588	CD	GLU	A	77	-17.440	41.739	69.427	1.00	100.00
ATOM	589	OE1	GLU	A	77	-16.537	41.435	70.211	1.00	100.00
ATOM	590	OE2	GLU	A	77	-18.712	41.799	69.770	1.00	100.00
ATOM	591	N	ARG	A	78	-13.452	44.344	67.000	1.00	54.17
ATOM	592	CA	ARG	A	78	-12.041	44.433	67.298	1.00	53.38
ATOM	593	C	ARG	A	78	-11.627	43.656	68.579	1.00	58.88
ATOM	594	O	ARG	A	78	-12.247	43.767	69.635	1.00	61.35
ATOM	595	CB	ARG	A	78	-11.571	45.891	67.367	1.00	41.96
ATOM	596	CG	ARG	A	78	-10.050	46.006	67.326	1.00	38.20
ATOM	597	CD	ARG	A	78	-9.537	47.411	67.551	1.00	44.73
ATOM	598	NE	ARG	A	78	-8.294	47.648	66.842	1.00	66.47
ATOM	599	CZ	ARG	A	78	-7.250	48.247	67.389	1.00	97.61
ATOM	600	NH1	ARG	A	78	-7.276	48.692	68.645	1.00	100.00
ATOM	601	NH2	ARG	A	78	-6.151	48.413	66.663	1.00	80.10
ATOM	602	N	GLN	A	79	-10.557	42.857	68.463	1.00	49.54
ATOM	603	CA	GLN	A	79	-9.995	42.115	69.566	1.00	47.71
ATOM	604	C	GLN	A	79	-8.664	42.789	69.865	1.00	49.77
ATOM	605	O	GLN	A	79	-7.626	42.421	69.333	1.00	52.63
ATOM	606	CB	GLN	A	79	-9.803	40.613	69.240	1.00	49.05
ATOM	607	CG	GLN	A	79	-11.109	39.794	69.339	1.00	57.32
ATOM	608	CD	GLN	A	79	-11.043	38.435	68.656	1.00	69.51
ATOM	609	OE1	GLN	A	79	-10.400	37.480	69.152	1.00	49.72

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ATOM    610  NE2 GLN A  79     -11.727  38.340  67.517  1.00 62.60
ATOM    611  N   SER A  80      -8.699  43.826  70.683  1.00 41.74
ATOM    612  CA  SER A  80      -7.490  44.543  71.022  1.00 37.90
ATOM    613  C   SER A  80      -6.437  44.559  69.920  1.00 35.98
ATOM    614  O   SER A  80      -6.736  44.939  68.801  1.00 34.52
ATOM    615  CB  SER A  80      -6.910  44.144  72.372  1.00 39.07
ATOM    616  OG  SER A  80      -7.255  42.803  72.684  1.00 61.32
ATOM    617  N   TYR A  81      -5.206  44.154  70.289  1.00 29.92
ATOM    618  CA  TYR A  81      -4.027  44.114  69.430  1.00 26.45
ATOM    619  C   TYR A  81      -4.163  43.116  68.285  1.00 30.82
ATOM    620  O   TYR A  81      -3.480  43.215  67.269  1.00 34.48
ATOM    621  CB  TYR A  81      -2.727  43.893  70.257  1.00 25.19
ATOM    622  CG  TYR A  81      -2.713  42.491  70.839  1.00 24.57
ATOM    623  CD1 TYR A  81      -3.327  42.247  72.066  1.00 27.27
ATOM    624  CD2 TYR A  81      -2.165  41.410  70.148  1.00 21.82
ATOM    625  CE1 TYR A  81      -3.380  40.975  72.632  1.00 26.49
ATOM    626  CE2 TYR A  81      -2.230  40.122  70.682  1.00 23.48
ATOM    627  CZ  TYR A  81      -2.827  39.908  71.930  1.00 38.28
ATOM    628  OH  TYR A  81      -2.889  38.653  72.493  1.00 42.17
ATOM    629  N   LYS A  82      -5.038  42.136  68.415  1.00 26.97
ATOM    630  CA  LYS A  82      -5.170  41.229  67.293  1.00 27.99
ATOM    631  C   LYS A  82      -5.867  41.898  66.072  1.00 38.90
ATOM    632  O   LYS A  82      -5.614  41.541  64.900  1.00 37.15
ATOM    633  CB  LYS A  82      -5.785  39.918  67.708  1.00 27.59
ATOM    634  CG  LYS A  82      -5.169  39.451  69.008  1.00 39.68
ATOM    635  CD  LYS A  82      -5.435  37.993  69.350  1.00 46.78
ATOM    636  CE  LYS A  82      -6.414  37.819  70.492  1.00 59.84
ATOM    637  NZ  LYS A  82      -7.097  36.523  70.452  1.00 63.48
ATOM    638  N   GLY A  83      -6.738  42.894  66.367  1.00 35.64
ATOM    639  CA  GLY A  83      -7.512  43.620  65.368  1.00 33.65
ATOM    640  C   GLY A  83      -8.866  42.925  65.111  1.00 32.95
ATOM    641  O   GLY A  83      -9.297  42.063  65.870  1.00 28.28
ATOM    642  N   SER A  84      -9.535  43.300  64.026  1.00 34.51
ATOM    643  CA  SER A  84     -10.839  42.742  63.673  1.00 36.13
ATOM    644  C   SER A  84     -10.796  41.724  62.549  1.00 40.65
ATOM    645  O   SER A  84     -10.173  41.893  61.501  1.00 39.77
ATOM    646  CB  SER A  84     -11.883  43.808  63.383  1.00 37.68
ATOM    647  OG  SER A  84     -11.812  44.832  64.352  1.00 45.14
ATOM    648  N   PRO A  85     -11.491  40.656  62.791  1.00 37.01
ATOM    649  CA  PRO A  85     -11.573  39.559  61.863  1.00 34.91
ATOM    650  C   PRO A  85     -12.459  39.946  60.712  1.00 35.92
ATOM    651  O   PRO A  85     -13.514  40.522  60.941  1.00 35.30
ATOM    652  CB  PRO A  85     -12.227  38.406  62.647  1.00 37.00
ATOM    653  CG  PRO A  85     -12.714  38.981  63.974  1.00 44.97
ATOM    654  CD  PRO A  85     -12.325  40.462  64.004  1.00 40.72
ATOM    655  N   MET A  86     -12.018  39.642  59.487  1.00 30.47
ATOM    656  CA  MET A  86     -12.756  39.960  58.275  1.00 28.55
ATOM    657  C   MET A  86     -13.165  38.683  57.552  1.00 40.49
ATOM    658  O   MET A  86     -12.338  38.015  56.954  1.00 39.69
ATOM    659  CB  MET A  86     -11.921  40.829  57.337  1.00 29.51
ATOM    660  CG  MET A  86     -12.750  41.242  56.136  1.00 37.40
ATOM    661  SD  MET A  86     -11.816  41.878  54.701  1.00 47.84
ATOM    662  CE  MET A  86     -13.244  42.527  53.805  1.00 46.52
ATOM    663  N   GLU A  87     -14.441  38.324  57.610  1.00 44.34
ATOM    664  CA  GLU A  87     -14.912  37.107  56.950  1.00 47.21
ATOM    665  C   GLU A  87     -15.495  37.352  55.560  1.00 51.53
ATOM    666  O   GLU A  87     -16.425  38.129  55.424  1.00 53.92
ATOM    667  CB  GLU A  87     -15.942  36.390  57.813  1.00 49.46
ATOM    668  CG  GLU A  87     -16.144  34.937  57.389  1.00 56.39
ATOM    669  CD  GLU A  87     -17.300  34.316  58.104  1.00 80.78
ATOM    670  OE1 GLU A  87     -18.439  34.738  57.994  1.00 86.69
ATOM    671  OE2 GLU A  87     -16.943  33.301  58.868  1.00 68.69
ATOM    672  N   ILE A  88     -14.942  36.659  54.544  1.00 43.84
ATOM    673  CA  ILE A  88     -15.332  36.765  53.145  1.00 40.15
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ATOM    674  C   ILE A  88     -16.145  35.610  52.613  1.00 46.72
ATOM    675  O   ILE A  88     -15.725  34.460  52.656  1.00 48.10
ATOM    676  CB  ILE A  88     -14.107  36.891  52.292  1.00 39.13
ATOM    677  CG1 ILE A  88     -13.328  38.146  52.696  1.00 38.40
ATOM    678  CG2 ILE A  88     -14.538  36.932  50.839  1.00 28.13
ATOM    679  CD1 ILE A  88     -11.944  38.200  52.051  1.00 30.07
ATOM    680  N   SER A  89     -17.314  35.931  52.077  1.00 45.16
ATOM    681  CA  SER A  89     -18.181  34.893  51.559  1.00 44.76
ATOM    682  C   SER A  89     -17.902  34.531  50.131  1.00 46.01
ATOM    683  O   SER A  89     -18.048  35.347  49.243  1.00 44.34
ATOM    684  CB  SER A  89     -19.657  35.121  51.827  1.00 51.87
ATOM    685  OG  SER A  89     -19.942  34.834  53.198  1.00 69.07
ATOM    686  N   LEU A  90     -17.494  33.279  49.914  1.00 46.43
ATOM    687  CA  LEU A  90     -17.204  32.804  48.575  1.00 46.93
ATOM    688  C   LEU A  90     -18.450  32.235  47.935  1.00 55.26
ATOM    689  O   LEU A  90     -19.210  31.476  48.556  1.00 54.94
ATOM    690  CB  LEU A  90     -16.080  31.750  48.521  1.00 46.14
ATOM    691  CG  LEU A  90     -15.262  31.607  49.792  1.00 50.78
ATOM    692  CD1 LEU A  90     -14.546  30.261  49.806  1.00 50.27
ATOM    693  CD2 LEU A  90     -14.219  32.708  49.863  1.00 55.52
ATOM    694  N   PRO A  91     -18.626  32.607  46.683  1.00 54.81
ATOM    695  CA  PRO A  91     -19.756  32.183  45.870  1.00 58.45
ATOM    696  C   PRO A  91     -19.585  30.782  45.254  1.00 67.78
ATOM    697  O   PRO A  91     -20.500  30.250  44.623  1.00 68.64
ATOM    698  CB  PRO A  91     -19.843  33.213  44.738  1.00 59.70
ATOM    699  CG  PRO A  91     -18.503  33.952  44.711  1.00 61.25
ATOM    700  CD  PRO A  91     -17.731  33.539  45.961  1.00 54.16
ATOM    701  N   ILE A  92     -18.413  30.177  45.416  1.00 64.82
ATOM    702  CA  ILE A  92     -18.210  28.863  44.850  1.00 65.03
ATOM    703  C   ILE A  92     -17.485  27.948  45.801  1.00 66.34
ATOM    704  O   ILE A  92     -16.258  27.984  45.865  1.00 70.20
ATOM    705  CB  ILE A  92     -17.433  28.927  43.547  1.00 69.56
ATOM    706  CG1 ILE A  92     -18.298  29.495  42.430  1.00 70.02
ATOM    707  CG2 ILE A  92     -16.975  27.517  43.171  1.00 71.86
ATOM    708  CD1 ILE A  92     -17.528  29.672  41.121  1.00 80.63
ATOM    709  N   ALA A  93     -18.219  27.115  46.534  1.00 54.40
ATOM    710  CA  ALA A  93     -17.526  26.247  47.452  1.00 51.74
ATOM    711  C   ALA A  93     -16.265  25.750  46.804  1.00 52.66
ATOM    712  O   ALA A  93     -16.288  25.319  45.662  1.00 49.87
ATOM    713  CB  ALA A  93     -18.367  25.101  47.968  1.00 52.76
ATOM    714  N   LEU A  94     -15.162  25.861  47.544  1.00 48.18
ATOM    715  CA  LEU A  94     -13.862  25.425  47.067  1.00 43.27
ATOM    716  C   LEU A  94     -13.566  24.066  47.581  1.00 43.98
ATOM    717  O   LEU A  94     -14.086  23.633  48.601  1.00 44.63
ATOM    718  CB  LEU A  94     -12.713  26.344  47.509  1.00 41.05
ATOM    719  CG  LEU A  94     -12.685  27.638  46.739  1.00 40.03
ATOM    720  CD1 LEU A  94     -11.272  28.200  46.751  1.00 36.88
ATOM    721  CD2 LEU A  94     -13.115  27.343  45.311  1.00 44.98
ATOM    722  N   SER A  95     -12.706  23.406  46.875  1.00 43.26
ATOM    723  CA  SER A  95     -12.321  22.074  47.256  1.00 43.76
ATOM    724  C   SER A  95     -10.807  21.991  47.344  1.00 38.58
ATOM    725  O   SER A  95     -10.087  22.944  46.975  1.00 36.78
ATOM    726  CB  SER A  95     -12.902  21.092  46.256  1.00 51.55
ATOM    727  OG  SER A  95     -14.299  21.305  46.156  1.00 62.74
ATOM    728  N   LYS A  96     -10.321  20.863  47.830  1.00 31.10
ATOM    729  CA  LYS A  96      -8.883  20.723  47.958  1.00 34.92
ATOM    730  C   LYS A  96      -8.058  21.238  46.777  1.00 45.63
ATOM    731  O   LYS A  96      -8.400  21.063  45.612  1.00 49.35
ATOM    732  CB  LYS A  96      -8.401  19.366  48.451  1.00 38.53
ATOM    733  CG  LYS A  96      -9.189  18.871  49.651  1.00 68.97
ATOM    734  CD  LYS A  96      -8.691  17.549  50.221  1.00 80.86
ATOM    735  CE  LYS A  96      -9.596  17.011  51.330  1.00 92.53
ATOM    736  NZ  LYS A  96      -9.049  15.833  52.029  1.00100.00
ATOM    737  N   ASN A  97      -6.944  21.873  47.108  1.00 41.92
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ATOM	738	CA	ASN	A	97	-6.009	22.403	46.139	1.00	40.91
ATOM	739	C	ASN	A	97	-6.606	23.348	45.088	1.00	42.64
ATOM	740	O	ASN	A	97	-5.963	23.681	44.068	1.00	38.69
ATOM	741	CB	ASN	A	97	-5.084	21.304	45.583	1.00	28.16
ATOM	742	CG	ASN	A	97	-4.327	20.568	46.677	1.00	52.21
ATOM	743	OD1	ASN	A	97	-3.089	20.627	46.744	1.00	55.30
ATOM	744	ND2	ASN	A	97	-5.060	19.858	47.533	1.00	53.87
ATOM	745	N	GLN	A	98	-7.833	23.791	45.382	1.00	36.59
ATOM	746	CA	GLN	A	98	-8.557	24.718	44.536	1.00	38.44
ATOM	747	C	GLN	A	98	-8.288	26.181	44.951	1.00	43.30
ATOM	748	O	GLN	A	98	-8.248	26.526	46.138	1.00	43.40
ATOM	749	CB	GLN	A	98	-10.064	24.395	44.575	1.00	42.26
ATOM	750	CG	GLN	A	98	-10.553	23.538	43.385	1.00	68.24
ATOM	751	CD	GLN	A	98	-12.008	23.778	43.010	1.00	95.57
ATOM	752	OE1	GLN	A	98	-12.890	22.935	43.278	1.00	86.92
ATOM	753	NE2	GLN	A	98	-12.271	24.935	42.393	1.00	95.48
ATOM	754	N	GLU	A	99	-8.089	27.062	43.973	1.00	39.70
ATOM	755	CA	GLU	A	99	-7.817	28.468	44.280	1.00	40.49
ATOM	756	C	GLU	A	99	-8.750	29.536	43.683	1.00	47.84
ATOM	757	O	GLU	A	99	-9.330	29.394	42.606	1.00	46.85
ATOM	758	CB	GLU	A	99	-6.361	28.866	43.951	1.00	40.24
ATOM	759	CG	GLU	A	99	-5.608	27.861	43.080	1.00	44.16
ATOM	760	CD	GLU	A	99	-4.120	28.119	42.990	1.00	65.64
ATOM	761	OE1	GLU	A	99	-3.636	29.062	42.376	1.00	73.95
ATOM	762	OE2	GLU	A	99	-3.395	27.210	43.614	1.00	55.99
ATOM	763	N	ILE	A	100	-8.848	30.643	44.418	1.00	43.55
ATOM	764	CA	ILE	A	100	-9.595	31.800	44.005	1.00	43.46
ATOM	765	C	ILE	A	100	-8.701	32.992	44.238	1.00	53.31
ATOM	766	O	ILE	A	100	-7.725	32.927	45.004	1.00	55.16
ATOM	767	CB	ILE	A	100	-10.881	32.068	44.773	1.00	46.65
ATOM	768	CG1	ILE	A	100	-10.762	31.640	46.227	1.00	50.76
ATOM	769	CG2	ILE	A	100	-12.111	31.486	44.106	1.00	46.76
ATOM	770	CD1	ILE	A	100	-9.959	32.620	47.087	1.00	64.36
ATOM	771	N	VAL	A	101	-9.060	34.076	43.580	1.00	48.20
ATOM	772	CA	VAL	A	101	-8.382	35.329	43.760	1.00	45.63
ATOM	773	C	VAL	A	101	-9.383	36.351	44.295	1.00	48.59
ATOM	774	O	VAL	A	101	-10.331	36.722	43.623	1.00	51.29
ATOM	775	CB	VAL	A	101	-7.461	35.793	42.633	1.00	45.06
ATOM	776	CG1	VAL	A	101	-7.693	35.000	41.378	1.00	43.25
ATOM	777	CG2	VAL	A	101	-7.609	37.289	42.395	1.00	45.02
ATOM	778	N	ILE	A	102	-9.182	36.738	45.546	1.00	41.15
ATOM	779	CA	ILE	A	102	-10.023	37.690	46.238	1.00	39.43
ATOM	780	C	ILE	A	102	-9.439	39.062	46.170	1.00	49.35
ATOM	781	O	ILE	A	102	-8.331	39.274	46.659	1.00	53.80
ATOM	782	CB	ILE	A	102	-10.097	37.319	47.694	1.00	39.19
ATOM	783	CG1	ILE	A	102	-10.180	35.800	47.809	1.00	35.28
ATOM	784	CG2	ILE	A	102	-11.300	37.992	48.341	1.00	35.25
ATOM	785	CD1	ILE	A	102	-10.962	35.392	49.044	1.00	47.09
ATOM	786	N	GLU	A	103	-10.192	39.984	45.572	1.00	43.20
ATOM	787	CA	GLU	A	103	-9.748	41.362	45.433	1.00	39.88
ATOM	788	C	GLU	A	103	-10.378	42.299	46.425	1.00	44.03
ATOM	789	O	GLU	A	103	-11.580	42.558	46.385	1.00	41.34
ATOM	790	CB	GLU	A	103	-9.950	41.930	44.047	1.00	39.11
ATOM	791	CG	GLU	A	103	-9.017	43.112	43.863	1.00	36.18
ATOM	792	CD	GLU	A	103	-9.150	43.666	42.485	1.00	61.93
ATOM	793	OE1	GLU	A	103	-10.157	44.234	42.100	1.00	69.89
ATOM	794	OE2	GLU	A	103	-8.087	43.457	41.744	1.00	76.18
ATOM	795	N	ILE	A	104	-9.534	42.797	47.322	1.00	42.69
ATOM	796	CA	ILE	A	104	-9.969	43.718	48.346	1.00	40.72
ATOM	797	C	ILE	A	104	-9.522	45.167	48.099	1.00	46.21
ATOM	798	O	ILE	A	104	-8.346	45.478	47.866	1.00	42.68
ATOM	799	CB	ILE	A	104	-9.578	43.283	49.754	1.00	41.75
ATOM	800	CG1	ILE	A	104	-10.006	41.855	50.032	1.00	39.85
ATOM	801	CG2	ILE	A	104	-10.225	44.222	50.768	1.00	41.53

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ATOM    802  CD1 ILE A 104      -8.839  40.995  50.485  1.00 34.17
ATOM    803  N   SER A 105     -10.506  46.056  48.173  1.00 47.94
ATOM    804  CA  SER A 105     -10.278  47.481  48.046  1.00 48.05
ATOM    805  C   SER A 105     -10.184  47.977  49.482  1.00 42.39
ATOM    806  O   SER A 105     -11.134  47.879  50.263  1.00 39.69
ATOM    807  CB  SER A 105     -11.399  48.180  47.290  1.00 53.77
ATOM    808  OG  SER A 105     -11.399  47.789  45.930  1.00 60.69
ATOM    809  N   PHE A 106      -9.020  48.445  49.857  1.00 35.07
ATOM    810  CA  PHE A 106      -8.844  48.890  51.223  1.00 34.98
ATOM    811  C   PHE A 106      -8.177  50.238  51.262  1.00 39.26
ATOM    812  O   PHE A 106      -7.607  50.730  50.265  1.00 34.24
ATOM    813  CB  PHE A 106      -8.015  47.864  52.060  1.00 36.05
ATOM    814  CG  PHE A 106      -6.581  47.815  51.556  1.00 37.24
ATOM    815  CD1 PHE A 106      -6.251  47.073  50.422  1.00 39.71
ATOM    816  CD2 PHE A 106      -5.579  48.579  52.161  1.00 36.44
ATOM    817  CE1 PHE A 106      -4.950  47.086  49.920  1.00 41.48
ATOM    818  CE2 PHE A 106      -4.273  48.609  51.672  1.00 38.19
ATOM    819  CZ  PHE A 106      -3.961  47.856  50.540  1.00 37.91
ATOM    820  N   GLU A 107      -8.284  50.794  52.453  1.00 40.64
ATOM    821  CA  GLU A 107      -7.711  52.064  52.848  1.00 43.81
ATOM    822  C   GLU A 107      -7.206  51.869  54.284  1.00 43.82
ATOM    823  O   GLU A 107      -7.933  51.303  55.121  1.00 38.38
ATOM    824  CB  GLU A 107      -8.737  53.234  52.753  1.00 46.93
ATOM    825  CG  GLU A 107      -8.107  54.637  52.467  1.00 67.21
ATOM    826  CD  GLU A 107      -9.086  55.715  52.042  1.00100.00
ATOM    827  OE1 GLU A 107     -10.208  55.504  51.599  1.00100.00
ATOM    828  OE2 GLU A 107      -8.631  56.938  52.221  1.00 93.72
ATOM    829  N   THR A 108      -5.963  52.294  54.551  1.00 39.12
ATOM    830  CA  THR A 108      -5.345  52.175  55.873  1.00 39.69
ATOM    831  C   THR A 108      -5.564  53.427  56.724  1.00 49.82
ATOM    832  O   THR A 108      -5.565  54.552  56.177  1.00 50.94
ATOM    833  CB  THR A 108      -3.810  52.095  55.722  1.00 40.40
ATOM    834  OG1 THR A 108      -3.360  53.226  54.981  1.00 32.22
ATOM    835  CG2 THR A 108      -3.371  50.802  55.042  1.00 46.43
ATOM    836  N   SER A 109      -5.698  53.217  58.065  1.00 42.02
ATOM    837  CA  SER A 109      -5.848  54.294  59.038  1.00 38.13
ATOM    838  C   SER A 109      -4.555  55.101  59.082  1.00 38.47
ATOM    839  O   SER A 109      -3.460  54.583  58.921  1.00 33.60
ATOM    840  CB  SER A 109      -6.166  53.759  60.437  1.00 41.44
ATOM    841  OG  SER A 109      -6.205  54.812  61.404  1.00 47.63
ATOM    842  N   PRO A 110      -4.655  56.392  59.308  1.00 41.64
ATOM    843  CA  PRO A 110      -3.419  57.116  59.393  1.00 40.75
ATOM    844  C   PRO A 110      -2.803  56.749  60.725  1.00 41.47
ATOM    845  O   PRO A 110      -1.676  57.080  61.009  1.00 42.30
ATOM    846  CB  PRO A 110      -3.721  58.605  59.298  1.00 42.09
ATOM    847  CG  PRO A 110      -5.224  58.719  59.132  1.00 48.77
ATOM    848  CD  PRO A 110      -5.811  57.318  59.269  1.00 44.58
ATOM    849  N   LYS A 111      -3.578  56.017  61.518  1.00 36.35
ATOM    850  CA  LYS A 111      -3.167  55.535  62.819  1.00 36.74
ATOM    851  C   LYS A 111      -2.669  54.083  62.720  1.00 40.19
ATOM    852  O   LYS A 111      -2.733  53.319  63.678  1.00 40.53
ATOM    853  CB  LYS A 111      -4.341  55.606  63.807  1.00 41.91
ATOM    854  CG  LYS A 111      -4.362  56.838  64.708  1.00 71.21
ATOM    855  CD  LYS A 111      -5.421  57.854  64.309  1.00 97.95
ATOM    856  CE  LYS A 111      -6.839  57.394  64.611  1.00100.00
ATOM    857  NZ  LYS A 111      -7.853  58.120  63.819  1.00100.00
ATOM    858  N   SER A 112      -2.184  53.670  61.550  1.00 36.84
ATOM    859  CA  SER A 112      -1.714  52.296  61.358  1.00 34.35
ATOM    860  C   SER A 112      -0.518  51.917  62.225  1.00 35.57
ATOM    861  O   SER A 112       0.533  52.548  62.166  1.00 32.49
ATOM    862  CB  SER A 112      -1.449  51.995  59.883  1.00 35.16
ATOM    863  OG  SER A 112      -0.682  50.814  59.762  1.00 31.94
ATOM    864  N   SER A 113      -0.666  50.872  63.033  1.00 31.84
ATOM    865  CA  SER A 113       0.445  50.460  63.866  1.00 29.27
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ATOM    866  C   SER A 113      1.601  49.927  63.040  1.00 33.37
ATOM    867  O   SER A 113      2.715  49.792  63.497  1.00 32.95
ATOM    868  CB  SER A 113      0.052  49.498  64.945  1.00 29.45
ATOM    869  OG  SER A 113      0.045  48.169  64.462  1.00 34.27
ATOM    870  N   ALA A 114      1.357  49.628  61.797  1.00 33.69
ATOM    871  CA  ALA A 114      2.437  49.134  60.981  1.00 34.05
ATOM    872  C   ALA A 114      3.239  50.287  60.388  1.00 37.83
ATOM    873  O   ALA A 114      4.411  50.149  60.033  1.00 37.72
ATOM    874  CB  ALA A 114      1.845  48.292  59.852  1.00 34.51
ATOM    875  N   LEU A 115      2.580  51.432  60.259  1.00 32.19
ATOM    876  CA  LEU A 115      3.201  52.595  59.662  1.00 30.48
ATOM    877  C   LEU A 115      3.509  53.745  60.565  1.00 35.32
ATOM    878  O   LEU A 115      2.902  54.012  61.604  1.00 35.25
ATOM    879  CB  LEU A 115      2.358  53.156  58.507  1.00 30.53
ATOM    880  CG  LEU A 115      1.787  52.064  57.602  1.00 35.51
ATOM    881  CD1 LEU A 115      0.812  52.710  56.637  1.00 35.12
ATOM    882  CD2 LEU A 115      2.903  51.387  56.821  1.00 33.88
ATOM    883  N   GLN A 116      4.490  54.457  60.096  1.00 34.00
ATOM    884  CA  GLN A 116      4.926  55.656  60.737  1.00 32.52
ATOM    885  C   GLN A 116      5.066  56.689  59.645  1.00 31.34
ATOM    886  O   GLN A 116      5.880  56.552  58.729  1.00 28.29
ATOM    887  CB  GLN A 116      6.232  55.540  61.496  1.00 32.66
ATOM    888  CG  GLN A 116      6.419  56.813  62.322  1.00 41.25
ATOM    889  CD  GLN A 116      7.777  56.897  62.952  1.00 50.08
ATOM    890  OE1 GLN A 116      8.515  55.905  63.017  1.00 55.36
ATOM    891  NE2 GLN A 116      8.090  58.081  63.438  1.00 38.23
ATOM    892  N   TRP A 117      4.210  57.680  59.748  1.00 26.66
ATOM    893  CA  TRP A 117      4.148  58.785  58.827  1.00 26.04
ATOM    894  C   TRP A 117      4.912  59.978  59.375  1.00 34.56
ATOM    895  O   TRP A 117      4.467  60.589  60.364  1.00 36.83
ATOM    896  CB  TRP A 117      2.669  59.188  58.630  1.00 23.15
ATOM    897  CG  TRP A 117      1.826  58.209  57.863  1.00 23.02
ATOM    898  CD1 TRP A 117      1.052  57.224  58.397  1.00 26.39
ATOM    899  CD2 TRP A 117      1.640  58.135  56.433  1.00 21.06
ATOM    900  NE1 TRP A 117      0.395  56.534  57.393  1.00 26.40
ATOM    901  CE2 TRP A 117      0.735  57.087  56.184  1.00 27.99
ATOM    902  CE3 TRP A 117      2.121  58.872  55.361  1.00 20.95
ATOM    903  CZ2 TRP A 117      0.352  56.753  54.886  1.00 28.21
ATOM    904  CZ3 TRP A 117      1.750  58.560  54.079  1.00 22.43
ATOM    905  CH2 TRP A 117      0.872  57.512  53.847  1.00 24.28
ATOM    906  N   LEU A 118      6.043  60.340  58.756  1.00 31.44
ATOM    907  CA  LEU A 118      6.745  61.506  59.276  1.00 36.67
ATOM    908  C   LEU A 118      6.584  62.774  58.432  1.00 46.93
ATOM    909  O   LEU A 118      6.434  62.705  57.210  1.00 51.17
ATOM    910  CB  LEU A 118      8.250  61.327  59.577  1.00 38.83
ATOM    911  CG  LEU A 118      8.881  59.939  59.398  1.00 44.33
ATOM    912  CD1 LEU A 118     10.392  60.065  59.569  1.00 42.12
ATOM    913  CD2 LEU A 118      8.351  58.950  60.426  1.00 49.99
ATOM    914  N   THR A 119      6.524  63.939  59.109  1.00 41.34
ATOM    915  CA  THR A 119      6.449  65.260  58.468  1.00 38.89
ATOM    916  C   THR A 119      7.847  65.633  58.034  1.00 40.14
ATOM    917  O   THR A 119      8.841  65.165  58.605  1.00 44.03
ATOM    918  CB  THR A 119      5.932  66.300  59.467  1.00 42.63
ATOM    919  OG1 THR A 119      6.994  66.605  60.362  1.00 50.01
ATOM    920  CG2 THR A 119      4.769  65.668  60.224  1.00 36.78
ATOM    921  N   PRO A 120      7.963  66.440  57.020  1.00 33.41
ATOM    922  CA  PRO A 120      9.275  66.781  56.517  1.00 33.18
ATOM    923  C   PRO A 120     10.260  67.209  57.599  1.00 38.27
ATOM    924  O   PRO A 120     11.433  66.829  57.566  1.00 34.42
ATOM    925  CB  PRO A 120      9.068  67.840  55.416  1.00 33.54
ATOM    926  CG  PRO A 120      7.582  67.823  55.097  1.00 34.86
ATOM    927  CD  PRO A 120      6.891  67.180  56.300  1.00 30.86
ATOM    928  N   GLU A 121      9.751  67.982  58.563  1.00 38.03
ATOM    929  CA  GLU A 121     10.534  68.474  59.681  1.00 41.03
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ATOM	930	C	GLU	A	121	11.212	67.361	60.411	1.00 50.88
ATOM	931	O	GLU	A	121	12.279	67.548	60.977	1.00 54.97
ATOM	932	CB	GLU	A	121	9.742	69.325	60.699	1.00 43.28
ATOM	933	CG	GLU	A	121	8.220	69.071	60.702	1.00 64.72
ATOM	934	CD	GLU	A	121	7.398	70.118	59.988	1.00 86.07
ATOM	935	OE1	GLU	A	121	7.007	71.131	60.538	1.00100.00
ATOM	936	OE2	GLU	A	121	7.108	69.803	58.739	1.00 59.72
ATOM	937	N	GLN	A	122	10.569	66.202	60.394	1.00 44.09
ATOM	938	CA	GLN	A	122	11.083	65.019	61.041	1.00 40.20
ATOM	939	C	GLN	A	122	12.170	64.373	60.232	1.00 47.73
ATOM	940	O	GLN	A	122	12.711	63.343	60.643	1.00 53.29
ATOM	941	CB	GLN	A	122	9.965	63.992	61.224	1.00 39.31
ATOM	942	CG	GLN	A	122	9.057	64.441	62.361	1.00 30.23
ATOM	943	CD	GLN	A	122	7.756	63.691	62.438	1.00 38.25
ATOM	944	OE1	GLN	A	122	6.899	63.804	61.548	1.00 53.34
ATOM	945	NE2	GLN	A	122	7.592	62.938	63.521	1.00 18.98
ATOM	946	N	THR	A	123	12.486	64.942	59.074	1.00 38.99
ATOM	947	CA	THR	A	123	13.490	64.319	58.229	1.00 36.00
ATOM	948	C	THR	A	123	14.755	65.034	58.264	1.00 35.30
ATOM	949	O	THR	A	123	14.842	66.074	58.875	1.00 34.95
ATOM	950	CB	THR	A	123	13.067	64.145	56.759	1.00 38.25
ATOM	951	OG1	THR	A	123	13.144	65.374	56.046	1.00 43.75
ATOM	952	CG2	THR	A	123	11.643	63.616	56.725	1.00 40.72
ATOM	953	N	SER	A	124	15.699	64.447	57.557	1.00 32.18
ATOM	954	CA	SER	A	124	17.025	64.996	57.442	1.00 33.71
ATOM	955	C	SER	A	124	17.007	66.216	56.553	1.00 39.04
ATOM	956	O	SER	A	124	17.537	67.268	56.883	1.00 39.07
ATOM	957	CB	SER	A	124	18.023	63.992	56.859	1.00 37.73
ATOM	958	OG	SER	A	124	18.359	62.978	57.796	1.00 36.28
ATOM	959	N	GLY	A	125	16.389	66.025	55.414	1.00 38.59
ATOM	960	CA	GLY	A	125	16.280	67.034	54.396	1.00 39.90
ATOM	961	C	GLY	A	125	15.290	68.094	54.749	1.00 46.83
ATOM	962	O	GLY	A	125	15.347	69.171	54.172	1.00 49.78
ATOM	963	N	LYS	A	126	14.391	67.788	55.678	1.00 41.09
ATOM	964	CA	LYS	A	126	13.396	68.761	56.126	1.00 41.26
ATOM	965	C	LYS	A	126	12.498	69.307	55.020	1.00 47.42
ATOM	966	O	LYS	A	126	11.617	70.141	55.279	1.00 48.94
ATOM	967	CB	LYS	A	126	14.024	69.936	56.894	1.00 41.98
ATOM	968	CG	LYS	A	126	15.094	69.555	57.913	1.00 45.84
ATOM	969	CD	LYS	A	126	14.535	68.838	59.135	1.00 58.74
ATOM	970	CE	LYS	A	126	15.612	68.500	60.151	1.00 72.12
ATOM	971	NZ	LYS	A	126	15.395	67.218	60.839	1.00 88.38
ATOM	972	N	GLU	A	127	12.722	68.858	53.792	1.00 41.82
ATOM	973	CA	GLU	A	127	11.921	69.344	52.708	1.00 41.98
ATOM	974	C	GLU	A	127	10.899	68.334	52.239	1.00 45.14
ATOM	975	O	GLU	A	127	9.994	68.683	51.496	1.00 46.95
ATOM	976	CB	GLU	A	127	12.727	70.015	51.543	1.00 44.39
ATOM	977	CG	GLU	A	127	13.198	71.499	51.820	1.00 57.99
ATOM	978	CD	GLU	A	127	12.331	72.659	51.301	1.00100.00
ATOM	979	OE1	GLU	A	127	11.652	72.611	50.286	1.00100.00
ATOM	980	OE2	GLU	A	127	12.387	73.758	52.054	1.00100.00
ATOM	981	N	HIS	A	128	11.027	67.077	52.653	1.00 39.18
ATOM	982	CA	HIS	A	128	10.068	66.072	52.210	1.00 39.43
ATOM	983	C	HIS	A	128	9.636	65.148	53.316	1.00 42.09
ATOM	984	O	HIS	A	128	10.366	64.955	54.281	1.00 45.34
ATOM	985	CB	HIS	A	128	10.628	65.194	51.097	1.00 42.16
ATOM	986	CG	HIS	A	128	10.947	65.936	49.854	1.00 47.24
ATOM	987	ND1	HIS	A	128	9.943	66.423	49.029	1.00 49.12
ATOM	988	CD2	HIS	A	128	12.159	66.262	49.322	1.00 51.13
ATOM	989	CE1	HIS	A	128	10.559	67.031	48.026	1.00 49.97
ATOM	990	NE2	HIS	A	128	11.888	66.953	48.166	1.00 50.87
ATOM	991	N	PRO	A	129	8.447	64.572	53.171	1.00 32.55
ATOM	992	CA	PRO	A	129	7.968	63.650	54.163	1.00 31.15
ATOM	993	C	PRO	A	129	8.636	62.328	53.900	1.00 34.90

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ATOM    994  O   PRO A 129       9.481  62.214  53.021  1.00 35.46
ATOM    995  CB  PRO A 129       6.466  63.490  53.986  1.00 31.94
ATOM    996  CG  PRO A 129       6.133  64.104  52.649  1.00 36.83
ATOM    997  CD  PRO A 129       7.384  64.850  52.185  1.00 32.71
ATOM    998  N   TYR A 130       8.248  61.342  54.659  1.00 29.47
ATOM    999  CA  TYR A 130       8.826  60.025  54.548  1.00 29.35
ATOM   1000  C   TYR A 130       7.856  59.046  55.156  1.00 31.83
ATOM   1001  O   TYR A 130       7.138  59.375  56.093  1.00 29.84
ATOM   1002  CB  TYR A 130      10.098  60.029  55.433  1.00 30.54
ATOM   1003  CG  TYR A 130      11.083  58.886  55.285  1.00 29.76
ATOM   1004  CD1 TYR A 130      10.845  57.630  55.845  1.00 26.16
ATOM   1005  CD2 TYR A 130      12.290  59.110  54.619  1.00 30.28
ATOM   1006  CE1 TYR A 130      11.795  56.621  55.721  1.00 17.87
ATOM   1007  CE2 TYR A 130      13.253  58.114  54.479  1.00 27.75
ATOM   1008  CZ  TYR A 130      12.983  56.866  55.031  1.00 25.76
ATOM   1009  OH  TYR A 130      13.899  55.864  54.894  1.00 40.52
ATOM   1010  N   LEU A 131       7.832  57.842  54.647  1.00 31.12
ATOM   1011  CA  LEU A 131       6.994  56.868  55.303  1.00 30.43
ATOM   1012  C   LEU A 131       7.691  55.568  55.289  1.00 33.91
ATOM   1013  O   LEU A 131       8.398  55.257  54.397  1.00 33.68
ATOM   1014  CB  LEU A 131       5.679  56.761  54.530  1.00 26.16
ATOM   1015  CG  LEU A 131       5.065  55.367  54.600  1.00 21.68
ATOM   1016  CD1 LEU A 131       4.163  55.206  55.797  1.00 17.56
ATOM   1017  CD2 LEU A 131       4.222  55.008  53.380  1.00 13.86
ATOM   1018  N   PHE A 132       7.533  54.828  56.348  1.00 29.24
ATOM   1019  CA  PHE A 132       8.129  53.527  56.323  1.00 33.44
ATOM   1020  C   PHE A 132       7.299  52.519  57.157  1.00 41.08
ATOM   1021  O   PHE A 132       6.344  52.889  57.837  1.00 46.05
ATOM   1022  CB  PHE A 132       9.621  53.670  56.791  1.00 36.40
ATOM   1023  CG  PHE A 132       9.763  53.895  58.256  1.00 38.11
ATOM   1024  CD1 PHE A 132       9.601  52.821  59.053  1.00 37.18
ATOM   1025  CD2 PHE A 132      10.123  55.158  58.803  1.00 43.89
ATOM   1026  CE1 PHE A 132       9.771  52.936  60.422  1.00 41.04
ATOM   1027  CE2 PHE A 132      10.289  55.258  60.174  1.00 47.72
ATOM   1028  CZ  PHE A 132      10.131  54.143  60.986  1.00 44.34
ATOM   1029  N   SER A 133       7.612  51.221  57.002  1.00 33.47
ATOM   1030  CA  SER A 133       6.744  50.228  57.629  1.00 29.86
ATOM   1031  C   SER A 133       7.499  49.221  58.504  1.00 31.53
ATOM   1032  O   SER A 133       8.724  49.146  58.531  1.00 33.16
ATOM   1033  CB  SER A 133       5.942  49.481  56.535  1.00 33.19
ATOM   1034  OG  SER A 133       6.757  48.480  55.926  1.00 50.66
ATOM   1035  N   GLN A 134       6.703  48.466  59.294  1.00 24.61
ATOM   1036  CA  GLN A 134       7.283  47.422  60.134  1.00 22.55
ATOM   1037  C   GLN A 134       6.268  46.321  60.398  1.00 27.28
ATOM   1038  O   GLN A 134       5.161  46.566  60.809  1.00 25.09
ATOM   1039  CB  GLN A 134       7.711  48.041  61.464  1.00 23.29
ATOM   1040  CG  GLN A 134       8.218  46.987  62.454  1.00 25.96
ATOM   1041  CD  GLN A 134       9.423  46.290  61.872  1.00 25.65
ATOM   1042  OE1 GLN A 134      10.296  46.876  61.263  1.00 26.36
ATOM   1043  NE2 GLN A 134       9.445  44.965  62.095  1.00 21.75
ATOM   1044  N   CYS A 135       6.435  45.124  59.820  1.00 29.60
ATOM   1045  CA  CYS A 135       5.291  44.220  59.755  1.00 32.30
ATOM   1046  C   CYS A 135       5.442  43.006  60.662  1.00 39.58
ATOM   1047  O   CYS A 135       4.597  42.144  60.739  1.00 40.94
ATOM   1048  CB  CYS A 135       5.098  43.794  58.320  1.00 35.40
ATOM   1049  SG  CYS A 135       3.976  44.922  57.445  1.00 41.22
ATOM   1050  N   GLN A 136       6.582  42.949  61.345  1.00 37.37
ATOM   1051  CA  GLN A 136       6.715  41.982  62.417  1.00 35.71
ATOM   1052  C   GLN A 136       6.589  42.645  63.797  1.00 31.90
ATOM   1053  O   GLN A 136       6.878  43.803  63.981  1.00 30.54
ATOM   1054  CB  GLN A 136       8.077  41.311  62.295  1.00 37.24
ATOM   1055  CG  GLN A 136       8.076  39.878  62.847  1.00 29.70
ATOM   1056  CD  GLN A 136       9.483  39.511  63.235  1.00 36.48
ATOM   1057  OE1 GLN A 136      10.366  40.328  63.356  1.00 24.49
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ATOM   1058  NE2 GLN A 136       9.665  38.201  63.443  1.00 22.19
ATOM   1059  N   ALA A 137       5.850  41.899  64.648  1.00 28.56
ATOM   1060  CA  ALA A 137       5.235  40.581  64.351  1.00 28.89
ATOM   1061  C   ALA A 137       3.860  40.503  63.630  1.00 31.83
ATOM   1062  O   ALA A 137       3.679  39.688  62.738  1.00 29.67
ATOM   1063  CB  ALA A 137       5.091  39.742  65.625  1.00 28.91
ATOM   1064  N   ILE A 138       2.863  41.285  64.070  1.00 27.07
ATOM   1065  CA  ILE A 138       1.553  41.176  63.445  1.00 23.90
ATOM   1066  C   ILE A 138       0.960  42.492  63.053  1.00 28.69
ATOM   1067  O   ILE A 138      -0.144  42.822  63.426  1.00 31.92
ATOM   1068  CB  ILE A 138       0.641  40.357  64.339  1.00 25.41
ATOM   1069  CG1 ILE A 138       0.871  40.811  65.801  1.00 27.32
ATOM   1070  CG2 ILE A 138       1.162  38.938  64.191  1.00 16.34
ATOM   1071  CD1 ILE A 138      -0.275  40.615  66.826  1.00 20.22
ATOM   1072  N   HIS A 139       1.718  43.223  62.265  1.00 24.05
ATOM   1073  CA  HIS A 139       1.322  44.511  61.824  1.00 24.05
ATOM   1074  C   HIS A 139       0.982  44.579  60.351  1.00 34.40
ATOM   1075  O   HIS A 139       0.539  45.625  59.888  1.00 35.89
ATOM   1076  CB  HIS A 139       2.439  45.519  62.173  1.00 24.63
ATOM   1077  CG  HIS A 139       2.689  45.619  63.657  1.00 27.97
ATOM   1078  ND1 HIS A 139       1.679  45.970  64.571  1.00 27.75
ATOM   1079  CD2 HIS A 139       3.835  45.437  64.356  1.00 28.42
ATOM   1080  CE1 HIS A 139       2.222  45.983  65.770  1.00 26.19
ATOM   1081  NE2 HIS A 139       3.517  45.668  65.671  1.00 27.42
ATOM   1082  N   CYS A 140       1.181  43.490  59.598  1.00 30.28
ATOM   1083  CA  CYS A 140       0.832  43.517  58.181  1.00 28.08
ATOM   1084  C   CYS A 140      -0.671  43.765  58.011  1.00 28.98
ATOM   1085  O   CYS A 140      -1.111  44.449  57.066  1.00 30.00
ATOM   1086  CB  CYS A 140       1.181  42.213  57.447  1.00 28.82
ATOM   1087  SG  CYS A 140       1.330  42.483  55.661  1.00 34.37
ATOM   1088  N   ARG A 141      -1.440  43.168  58.949  1.00 20.78
ATOM   1089  CA  ARG A 141      -2.884  43.252  58.996  1.00 20.33
ATOM   1090  C   ARG A 141      -3.286  44.684  59.003  1.00 32.37
ATOM   1091  O   ARG A 141      -4.355  45.032  58.510  1.00 35.81
ATOM   1092  CB  ARG A 141      -3.557  42.498  60.156  1.00 14.60
ATOM   1093  CG  ARG A 141      -3.081  42.891  61.568  1.00 20.94
ATOM   1094  CD  ARG A 141      -3.576  41.978  62.715  1.00 19.99
ATOM   1095  NE  ARG A 141      -2.911  40.690  62.786  1.00 18.24
ATOM   1096  CZ  ARG A 141      -3.140  39.707  63.648  1.00 18.77
ATOM   1097  NH1 ARG A 141      -4.029  39.739  64.634  1.00 20.76
ATOM   1098  NH2 ARG A 141      -2.415  38.640  63.508  1.00 24.20
ATOM   1099  N   ALA A 142      -2.408  45.511  59.580  1.00 28.35
ATOM   1100  CA  ALA A 142      -2.668  46.940  59.657  1.00 27.60
ATOM   1101  C   ALA A 142      -2.369  47.652  58.345  1.00 34.33
ATOM   1102  O   ALA A 142      -2.620  48.835  58.203  1.00 34.36
ATOM   1103  CB  ALA A 142      -1.994  47.616  60.843  1.00 27.67
ATOM   1104  N   ILE A 143      -1.824  46.922  57.382  1.00 32.39
ATOM   1105  CA  ILE A 143      -1.537  47.499  56.099  1.00 30.38
ATOM   1106  C   ILE A 143      -2.520  46.994  55.067  1.00 37.79
ATOM   1107  O   ILE A 143      -2.885  47.709  54.152  1.00 42.65
ATOM   1108  CB  ILE A 143      -0.142  47.228  55.613  1.00 32.06
ATOM   1109  CG1 ILE A 143       0.827  48.062  56.414  1.00 31.71
ATOM   1110  CG2 ILE A 143      -0.074  47.654  54.143  1.00 34.02
ATOM   1111  CD1 ILE A 143       2.258  47.774  55.988  1.00 42.10
ATOM   1112  N   LEU A 144      -2.939  45.749  55.218  1.00 32.50
ATOM   1113  CA  LEU A 144      -3.873  45.142  54.291  1.00 32.36
ATOM   1114  C   LEU A 144      -4.435  43.838  54.849  1.00 40.36
ATOM   1115  O   LEU A 144      -3.959  43.278  55.852  1.00 33.27
ATOM   1116  CB  LEU A 144      -3.250  44.936  52.894  1.00 31.58
ATOM   1117  CG  LEU A 144      -1.923  44.170  52.917  1.00 33.31
ATOM   1118  CD1 LEU A 144      -2.147  42.770  52.352  1.00 32.07
ATOM   1119  CD2 LEU A 144      -0.836  44.897  52.110  1.00 28.67
ATOM   1120  N   PRO A 145      -5.490  43.347  54.213  1.00 40.02
ATOM   1121  CA  PRO A 145      -6.080  42.129  54.715  1.00 37.86
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ATOM   1122  C   PRO A 145      -5.264  40.941  54.286  1.00 37.87
ATOM   1123  O   PRO A 145      -4.819  40.831  53.144  1.00 35.27
ATOM   1124  CB  PRO A 145      -7.530  42.080  54.220  1.00 38.81
ATOM   1125  CG  PRO A 145      -7.778  43.393  53.492  1.00 41.34
ATOM   1126  CD  PRO A 145      -6.432  44.093  53.341  1.00 36.69
ATOM   1127  N   CYS A 146      -5.041  40.056  55.233  1.00 36.18
ATOM   1128  CA  CYS A 146      -4.250  38.882  54.958  1.00 35.60
ATOM   1129  C   CYS A 146      -4.358  37.859  56.069  1.00 33.04
ATOM   1130  O   CYS A 146      -5.067  38.062  57.050  1.00 30.78
ATOM   1131  CB  CYS A 146      -2.761  39.287  54.813  1.00 36.08
ATOM   1132  SG  CYS A 146      -2.087  40.108  56.302  1.00 39.43
ATOM   1133  N   GLN A 147      -3.637  36.755  55.883  1.00 29.33
ATOM   1134  CA  GLN A 147      -3.517  35.703  56.875  1.00 29.71
ATOM   1135  C   GLN A 147      -2.254  36.131  57.628  1.00 38.75
ATOM   1136  O   GLN A 147      -1.141  35.926  57.135  1.00 40.79
ATOM   1137  CB  GLN A 147      -3.322  34.352  56.206  1.00 28.99
ATOM   1138  CG  GLN A 147      -4.672  33.707  55.894  1.00 25.73
ATOM   1139  CD  GLN A 147      -4.562  32.532  54.960  1.00 39.92
ATOM   1140  OE1 GLN A 147      -4.217  32.668  53.775  1.00 43.89
ATOM   1141  NE2 GLN A 147      -4.828  31.368  55.499  1.00 26.36
ATOM   1142  N   ASP A 148      -2.425  36.834  58.765  1.00 32.68
ATOM   1143  CA  ASP A 148      -1.287  37.362  59.474  1.00 33.50
ATOM   1144  C   ASP A 148      -0.629  36.377  60.371  1.00 33.13
ATOM   1145  O   ASP A 148      -0.622  36.563  61.584  1.00 31.30
ATOM   1146  CB  ASP A 148      -1.633  38.642  60.253  1.00 37.78
ATOM   1147  CG  ASP A 148      -0.535  39.666  60.332  1.00 45.10
ATOM   1148  OD1 ASP A 148       0.564  39.540  59.836  1.00 47.89
ATOM   1149  OD2 ASP A 148      -0.913  40.737  60.952  1.00 48.63
ATOM   1150  N   THR A 149      -0.080  35.345  59.742  1.00 29.15
ATOM   1151  CA  THR A 149       0.584  34.251  60.422  1.00 28.25
ATOM   1152  C   THR A 149       1.805  33.831  59.625  1.00 34.92
ATOM   1153  O   THR A 149       1.757  33.764  58.410  1.00 34.47
ATOM   1154  CB  THR A 149      -0.403  33.087  60.674  1.00 24.79
ATOM   1155  OG1 THR A 149       0.241  32.059  61.352  1.00 37.15
ATOM   1156  CG2 THR A 149      -0.905  32.527  59.345  1.00 26.56
ATOM   1157  N   PRO A 150       2.910  33.575  60.323  1.00 34.69
ATOM   1158  CA  PRO A 150       4.142  33.217  59.659  1.00 31.06
ATOM   1159  C   PRO A 150       4.087  31.813  59.131  1.00 36.66
ATOM   1160  O   PRO A 150       4.995  31.356  58.450  1.00 36.37
ATOM   1161  CB  PRO A 150       5.245  33.327  60.712  1.00 31.18
ATOM   1162  CG  PRO A 150       4.570  33.471  62.077  1.00 36.95
ATOM   1163  CD  PRO A 150       3.078  33.589  61.823  1.00 34.62
ATOM   1164  N   SER A 151       2.992  31.150  59.452  1.00 31.62
ATOM   1165  CA  SER A 151       2.778  29.791  59.029  1.00 27.35
ATOM   1166  C   SER A 151       2.357  29.738  57.564  1.00 32.97
ATOM   1167  O   SER A 151       2.344  28.703  56.928  1.00 34.25
ATOM   1168  CB  SER A 151       1.714  29.203  59.905  1.00 25.95
ATOM   1169  OG  SER A 151       0.483  29.685  59.439  1.00 49.35
ATOM   1170  N   VAL A 152       1.997  30.887  57.024  1.00 34.36
ATOM   1171  CA  VAL A 152       1.595  31.015  55.623  1.00 33.74
ATOM   1172  C   VAL A 152       2.705  31.764  54.847  1.00 37.45
ATOM   1173  O   VAL A 152       3.295  32.761  55.313  1.00 37.63
ATOM   1174  CB  VAL A 152       0.203  31.697  55.427  1.00 32.61
ATOM   1175  CG1 VAL A 152      -0.184  31.767  53.963  1.00 31.50
ATOM   1176  CG2 VAL A 152      -0.915  30.975  56.149  1.00 31.29
ATOM   1177  N   LYS A 153       2.999  31.289  53.654  1.00 26.98
ATOM   1178  CA  LYS A 153       4.002  31.927  52.866  1.00 25.81
ATOM   1179  C   LYS A 153       3.469  32.141  51.473  1.00 33.94
ATOM   1180  O   LYS A 153       2.826  31.251  50.936  1.00 32.91
ATOM   1181  CB  LYS A 153       5.252  31.091  52.841  1.00 24.70
ATOM   1182  CG  LYS A 153       6.383  31.760  53.583  1.00 34.68
ATOM   1183  CD  LYS A 153       7.641  30.893  53.616  1.00 39.37
ATOM   1184  CE  LYS A 153       8.121  30.506  55.015  1.00 29.09
ATOM   1185  NZ  LYS A 153       9.556  30.152  55.112  1.00 26.03
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ATOM	1186	N	LEU	A	154	3.732	33.321	50.896	1.00 32.13
ATOM	1187	CA	LEU	A	154	3.285	33.639	49.544	1.00 30.67
ATOM	1188	C	LEU	A	154	4.279	34.475	48.789	1.00 40.67
ATOM	1189	O	LEU	A	154	5.264	35.000	49.344	1.00 42.56
ATOM	1190	CB	LEU	A	154	1.966	34.432	49.515	1.00 30.10
ATOM	1191	CG	LEU	A	154	2.084	35.793	50.207	1.00 35.20
ATOM	1192	CD1	LEU	A	154	0.989	36.716	49.690	1.00 37.21
ATOM	1193	CD2	LEU	A	154	1.934	35.608	51.715	1.00 33.07
ATOM	1194	N	THR	A	155	3.963	34.610	47.499	1.00 37.82
ATOM	1195	CA	THR	A	155	4.728	35.449	46.596	1.00 38.44
ATOM	1196	C	THR	A	155	3.934	36.730	46.389	1.00 41.52
ATOM	1197	O	THR	A	155	2.738	36.775	46.674	1.00 43.95
ATOM	1198	CB	THR	A	155	5.041	34.814	45.230	1.00 36.99
ATOM	1199	OG1	THR	A	155	3.886	34.281	44.584	1.00 32.59
ATOM	1200	CG2	THR	A	155	6.133	33.790	45.404	1.00 18.24
ATOM	1201	N	TYR	A	156	4.563	37.768	45.892	1.00 33.87
ATOM	1202	CA	TYR	A	156	3.835	39.003	45.683	1.00 32.49
ATOM	1203	C	TYR	A	156	4.509	39.922	44.717	1.00 37.91
ATOM	1204	O	TYR	A	156	5.725	39.940	44.562	1.00 39.04
ATOM	1205	CB	TYR	A	156	3.534	39.795	46.983	1.00 31.16
ATOM	1206	CG	TYR	A	156	4.642	40.731	47.471	1.00 28.94
ATOM	1207	CD1	TYR	A	156	4.817	42.021	46.969	1.00 30.33
ATOM	1208	CD2	TYR	A	156	5.525	40.303	48.465	1.00 30.43
ATOM	1209	CE1	TYR	A	156	5.829	42.853	47.459	1.00 36.89
ATOM	1210	CE2	TYR	A	156	6.553	41.104	48.960	1.00 31.47
ATOM	1211	CZ	TYR	A	156	6.690	42.396	48.462	1.00 43.34
ATOM	1212	OH	TYR	A	156	7.701	43.180	48.956	1.00 36.86
ATOM	1213	N	THR	A	157	3.657	40.689	44.101	1.00 36.75
ATOM	1214	CA	THR	A	157	4.036	41.691	43.171	1.00 38.49
ATOM	1215	C	THR	A	157	3.346	42.942	43.611	1.00 42.61
ATOM	1216	O	THR	A	157	2.228	42.913	44.143	1.00 38.45
ATOM	1217	CB	THR	A	157	3.631	41.316	41.751	1.00 39.73
ATOM	1218	OG1	THR	A	157	2.380	40.655	41.803	1.00 55.71
ATOM	1219	CG2	THR	A	157	4.680	40.370	41.212	1.00 26.71
ATOM	1220	N	ALA	A	158	4.037	44.025	43.404	1.00 41.36
ATOM	1221	CA	ALA	A	158	3.488	45.273	43.789	1.00 41.08
ATOM	1222	C	ALA	A	158	3.869	46.401	42.839	1.00 50.77
ATOM	1223	O	ALA	A	158	4.919	46.390	42.179	1.00 53.47
ATOM	1224	CB	ALA	A	158	3.910	45.570	45.212	1.00 39.87
ATOM	1225	N	GLU	A	159	2.974	47.376	42.788	1.00 43.90
ATOM	1226	CA	GLU	A	159	3.107	48.604	42.023	1.00 42.27
ATOM	1227	C	GLU	A	159	2.451	49.705	42.843	1.00 42.17
ATOM	1228	O	GLU	A	159	1.257	49.630	43.227	1.00 41.00
ATOM	1229	CB	GLU	A	159	2.641	48.521	40.571	1.00 43.72
ATOM	1230	CG	GLU	A	159	1.943	47.197	40.255	1.00 62.90
ATOM	1231	CD	GLU	A	159	1.502	47.156	38.835	1.00 91.28
ATOM	1232	OE1	GLU	A	159	2.202	46.696	37.955	1.00 77.84
ATOM	1233	OE2	GLU	A	159	0.322	47.707	38.644	1.00100.00
ATOM	1234	N	VAL	A	160	3.263	50.686	43.197	1.00 34.67
ATOM	1235	CA	VAL	A	160	2.738	51.717	44.044	1.00 36.57
ATOM	1236	C	VAL	A	160	3.024	53.091	43.533	1.00 43.02
ATOM	1237	O	VAL	A	160	4.121	53.380	43.050	1.00 42.71
ATOM	1238	CB	VAL	A	160	3.180	51.530	45.500	1.00 40.73
ATOM	1239	CG1	VAL	A	160	3.988	50.239	45.644	1.00 38.56
ATOM	1240	CG2	VAL	A	160	4.006	52.728	45.963	1.00 40.46
ATOM	1241	N	SER	A	161	2.002	53.922	43.653	1.00 41.79
ATOM	1242	CA	SER	A	161	2.076	55.292	43.185	1.00 42.07
ATOM	1243	C	SER	A	161	2.532	56.204	44.270	1.00 44.28
ATOM	1244	O	SER	A	161	2.047	56.121	45.403	1.00 43.60
ATOM	1245	CB	SER	A	161	0.751	55.801	42.635	1.00 43.32
ATOM	1246	OG	SER	A	161	0.971	56.850	41.726	1.00 49.40
ATOM	1247	N	VAL	A	162	3.447	57.080	43.896	1.00 36.49
ATOM	1248	CA	VAL	A	162	3.979	58.019	44.838	1.00 34.99
ATOM	1249	C	VAL	A	162	4.273	59.319	44.148	1.00 42.57

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ATOM   1250  O   VAL A 162       4.470  59.354  42.932  1.00 44.41
ATOM   1251  CB  VAL A 162       5.300  57.498  45.402  1.00 35.97
ATOM   1252  CG1 VAL A 162       5.084  56.219  46.188  1.00 36.12
ATOM   1253  CG2 VAL A 162       6.222  57.194  44.239  1.00 35.42
ATOM   1254  N   PRO A 163       4.332  60.377  44.942  1.00 32.95
ATOM   1255  CA  PRO A 163       4.664  61.662  44.400  1.00 31.07
ATOM   1256  C   PRO A 163       5.966  61.496  43.652  1.00 39.67
ATOM   1257  O   PRO A 163       6.919  60.892  44.142  1.00 42.78
ATOM   1258  CB  PRO A 163       4.780  62.562  45.618  1.00 31.62
ATOM   1259  CG  PRO A 163       3.946  61.893  46.714  1.00 33.93
ATOM   1260  CD  PRO A 163       3.652  60.480  46.259  1.00 28.53
ATOM   1261  N   LYS A 164       5.962  61.978  42.436  1.00 38.52
ATOM   1262  CA  LYS A 164       7.086  61.860  41.539  1.00 39.97
ATOM   1263  C   LYS A 164       8.451  62.222  42.088  1.00 42.75
ATOM   1264  O   LYS A 164       9.453  61.708  41.593  1.00 44.47
ATOM   1265  CB  LYS A 164       6.828  62.479  40.177  1.00 44.67
ATOM   1266  CG  LYS A 164       6.004  63.758  40.257  1.00 78.05
ATOM   1267  CD  LYS A 164       6.651  64.918  39.497  1.00100.00
ATOM   1268  CE  LYS A 164       6.016  66.289  39.772  1.00100.00
ATOM   1269  NZ  LYS A 164       6.679  67.075  40.835  1.00100.00
ATOM   1270  N   GLU A 165       8.519  63.097  43.082  1.00 37.25
ATOM   1271  CA  GLU A 165       9.814  63.489  43.665  1.00 39.56
ATOM   1272  C   GLU A 165      10.333  62.462  44.677  1.00 46.39
ATOM   1273  O   GLU A 165      11.531  62.318  44.927  1.00 48.93
ATOM   1274  CB  GLU A 165       9.797  64.902  44.297  1.00 42.10
ATOM   1275  CG  GLU A 165       8.602  65.156  45.257  1.00 58.16
ATOM   1276  CD  GLU A 165       7.214  64.970  44.664  1.00 88.01
ATOM   1277  OE1 GLU A 165       6.994  64.757  43.475  1.00 79.46
ATOM   1278  OE2 GLU A 165       6.266  65.050  45.575  1.00 70.27
ATOM   1279  N   LEU A 166       9.398  61.733  45.265  1.00 40.39
ATOM   1280  CA  LEU A 166       9.696  60.733  46.254  1.00 36.56
ATOM   1281  C   LEU A 166       9.934  59.377  45.640  1.00 47.57
ATOM   1282  O   LEU A 166       9.366  59.080  44.581  1.00 52.86
ATOM   1283  CB  LEU A 166       8.525  60.630  47.250  1.00 31.92
ATOM   1284  CG  LEU A 166       8.315  61.912  48.057  1.00 29.18
ATOM   1285  CD1 LEU A 166       7.363  61.590  49.189  1.00 25.96
ATOM   1286  CD2 LEU A 166       9.635  62.467  48.622  1.00 23.78
ATOM   1287  N   VAL A 167      10.769  58.564  46.328  1.00 34.75
ATOM   1288  CA  VAL A 167      11.077  57.218  45.908  1.00 30.00
ATOM   1289  C   VAL A 167      10.332  56.229  46.771  1.00 38.80
ATOM   1290  O   VAL A 167       9.902  56.532  47.879  1.00 40.91
ATOM   1291  CB  VAL A 167      12.549  56.860  46.048  1.00 31.28
ATOM   1292  CG1 VAL A 167      12.854  55.542  45.329  1.00 28.20
ATOM   1293  CG2 VAL A 167      13.456  57.964  45.565  1.00 31.06
ATOM   1294  N   ALA A 168      10.217  55.019  46.257  1.00 36.46
ATOM   1295  CA  ALA A 168       9.584  53.935  46.979  1.00 35.14
ATOM   1296  C   ALA A 168      10.418  52.662  46.836  1.00 43.27
ATOM   1297  O   ALA A 168      10.889  52.343  45.733  1.00 44.74
ATOM   1298  CB  ALA A 168       8.149  53.700  46.550  1.00 34.20
ATOM   1299  N   LEU A 169      10.603  51.960  47.975  1.00 35.27
ATOM   1300  CA  LEU A 169      11.323  50.696  48.069  1.00 29.39
ATOM   1301  C   LEU A 169      10.491  49.635  48.797  1.00 33.87
ATOM   1302  O   LEU A 169       9.604  49.918  49.613  1.00 31.21
ATOM   1303  CB  LEU A 169      12.721  50.835  48.656  1.00 28.62
ATOM   1304  CG  LEU A 169      13.593  51.810  47.891  1.00 35.90
ATOM   1305  CD1 LEU A 169      14.953  51.819  48.558  1.00 39.38
ATOM   1306  CD2 LEU A 169      13.765  51.394  46.432  1.00 37.35
ATOM   1307  N   MET A 170      10.758  48.381  48.479  1.00 34.23
ATOM   1308  CA  MET A 170      10.012  47.291  49.069  1.00 31.07
ATOM   1309  C   MET A 170      10.874  46.083  49.287  1.00 34.13
ATOM   1310  O   MET A 170      11.995  45.973  48.775  1.00 35.20
ATOM   1311  CB  MET A 170       8.842  46.882  48.154  1.00 31.95
ATOM   1312  CG  MET A 170       7.751  47.934  48.116  1.00 33.13
ATOM   1313  SD  MET A 170       6.105  47.253  47.815  1.00 34.54
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ATOM	1314	CE	MET	A	170	5.820	46.349	49.363	1.00	32.25
ATOM	1315	N	SER	A	171	10.332	45.165	50.057	1.00	28.20
ATOM	1316	CA	SER	A	171	11.064	43.953	50.297	1.00	28.47
ATOM	1317	C	SER	A	171	10.929	43.054	49.049	1.00	32.01
ATOM	1318	O	SER	A	171	10.396	41.958	49.089	1.00	30.93
ATOM	1319	CB	SER	A	171	10.662	43.265	51.606	1.00	30.93
ATOM	1320	OG	SER	A	171	9.297	42.920	51.581	1.00	32.90
ATOM	1321	N	ALA	A	172	11.401	43.543	47.912	1.00	28.84
ATOM	1322	CA	ALA	A	172	11.286	42.773	46.691	1.00	29.48
ATOM	1323	C	ALA	A	172	12.241	43.258	45.644	1.00	37.63
ATOM	1324	O	ALA	A	172	13.060	44.147	45.881	1.00	35.07
ATOM	1325	CB	ALA	A	172	9.884	42.969	46.120	1.00	29.48
ATOM	1326	N	ILE	A	173	12.104	42.686	44.452	1.00	39.49
ATOM	1327	CA	ILE	A	173	12.966	43.120	43.382	1.00	38.64
ATOM	1328	C	ILE	A	173	12.418	44.343	42.648	1.00	44.83
ATOM	1329	O	ILE	A	173	11.269	44.394	42.193	1.00	40.97
ATOM	1330	CB	ILE	A	173	13.549	42.027	42.479	1.00	38.79
ATOM	1331	CG1	ILE	A	173	14.258	40.970	43.302	1.00	37.40
ATOM	1332	CG2	ILE	A	173	14.606	42.621	41.570	1.00	38.88
ATOM	1333	CD1	ILE	A	173	15.770	41.069	43.193	1.00	25.93
ATOM	1334	N	ARG	A	174	13.286	45.345	42.584	1.00	43.21
ATOM	1335	CA	ARG	A	174	12.997	46.567	41.917	1.00	42.34
ATOM	1336	C	ARG	A	174	12.630	46.173	40.516	1.00	47.54
ATOM	1337	O	ARG	A	174	13.478	45.667	39.770	1.00	42.08
ATOM	1338	CB	ARG	A	174	14.254	47.422	41.937	1.00	42.47
ATOM	1339	CG	ARG	A	174	14.231	48.450	43.075	1.00	53.40
ATOM	1340	CD	ARG	A	174	15.617	48.917	43.515	1.00	33.80
ATOM	1341	NE	ARG	A	174	16.036	50.083	42.756	1.00	53.32
ATOM	1342	CZ	ARG	A	174	17.221	50.208	42.181	1.00	97.11
ATOM	1343	NH1	ARG	A	174	18.132	49.243	42.266	1.00	100.00
ATOM	1344	NH2	ARG	A	174	17.503	51.321	41.489	1.00	100.00
ATOM	1345	N	ASP	A	175	11.356	46.356	40.195	1.00	51.12
ATOM	1346	CA	ASP	A	175	10.858	45.981	38.882	1.00	53.89
ATOM	1347	C	ASP	A	175	10.778	47.128	37.885	1.00	58.32
ATOM	1348	O	ASP	A	175	10.455	46.901	36.727	1.00	56.00
ATOM	1349	CB	ASP	A	175	9.533	45.186	38.948	1.00	57.16
ATOM	1350	CG	ASP	A	175	9.196	44.446	37.675	1.00	81.25
ATOM	1351	OD1	ASP	A	175	10.034	44.118	36.851	1.00	83.53
ATOM	1352	OD2	ASP	A	175	7.910	44.176	37.558	1.00	92.45
ATOM	1353	N	GLY	A	176	11.062	48.356	38.331	1.00	58.24
ATOM	1354	CA	GLY	A	176	11.021	49.498	37.438	1.00	57.71
ATOM	1355	C	GLY	A	176	9.969	50.546	37.773	1.00	58.98
ATOM	1356	O	GLY	A	176	9.090	50.371	38.620	1.00	52.04
ATOM	1357	N	GLU	A	177	10.110	51.649	37.050	1.00	63.72
ATOM	1358	CA	GLU	A	177	9.267	52.812	37.172	1.00	67.79
ATOM	1359	C	GLU	A	177	8.874	53.388	35.817	1.00	86.22
ATOM	1360	O	GLU	A	177	9.614	53.364	34.830	1.00	91.14
ATOM	1361	CB	GLU	A	177	9.986	53.902	38.006	1.00	68.25
ATOM	1362	CG	GLU	A	177	11.432	54.145	37.519	1.00	71.58
ATOM	1363	CD	GLU	A	177	12.183	55.088	38.404	1.00	85.08
ATOM	1364	OE1	GLU	A	177	13.045	54.733	39.198	1.00	100.00
ATOM	1365	OE2	GLU	A	177	11.765	56.316	38.264	1.00	56.71
ATOM	1366	N	THR	A	178	7.671	53.924	35.835	1.00	84.76
ATOM	1367	CA	THR	A	178	6.684	54.686	35.042	1.00	84.81
ATOM	1368	C	THR	A	178	6.024	55.810	35.855	1.00	90.37
ATOM	1369	O	THR	A	178	5.664	55.655	36.996	1.00	91.10
ATOM	1370	CB	THR	A	178	5.618	53.713	34.561	1.00	89.82
ATOM	1371	OG1	THR	A	178	5.283	52.830	35.636	1.00	80.25
ATOM	1372	CG2	THR	A	178	6.161	52.898	33.396	1.00	93.46
ATOM	1373	N	PRO	A	179	5.921	56.984	35.217	1.00	87.05
ATOM	1374	CA	PRO	A	179	5.365	58.187	35.845	1.00	86.61
ATOM	1375	C	PRO	A	179	3.857	58.419	35.531	1.00	89.04
ATOM	1376	O	PRO	A	179	3.444	59.516	35.140	1.00	91.15
ATOM	1377	CB	PRO	A	179	6.176	59.345	35.301	1.00	88.63

ATOM	1378	CG	PRO	A	179	6.657	58.947	33.895	1.00 92.62
ATOM	1379	CD	PRO	A	179	6.426	57.345	33.902	1.00 87.63
ATOM	1380	N	ASP	A	180	3.020	57.347	35.694	1.00 82.31
ATOM	1381	CA	ASP	A	180	1.616	57.568	35.310	1.00 81.19
ATOM	1382	C	ASP	A	180	0.629	56.743	36.166	1.00 90.72
ATOM	1383	O	ASP	A	180	0.533	55.519	36.072	1.00 91.13
ATOM	1384	CB	ASP	A	180	1.458	57.196	33.827	1.00 82.12
ATOM	1385	CG	ASP	A	180	0.087	57.651	33.327	1.00 95.94
ATOM	1386	OD1	ASP	A	180	-0.155	58.858	33.337	1.00100.00
ATOM	1387	OD2	ASP	A	180	-0.714	56.801	32.946	1.00 94.36
ATOM	1388	N	PRO	A	181	-0.060	57.456	37.086	1.00 92.45
ATOM	1389	CA	PRO	A	181	-1.212	56.934	37.795	1.00 92.02
ATOM	1390	C	PRO	A	181	-2.519	57.566	37.284	1.00100.00
ATOM	1391	O	PRO	A	181	-2.605	58.114	36.192	1.00100.00
ATOM	1392	CB	PRO	A	181	-1.014	57.340	39.210	1.00 92.48
ATOM	1393	CG	PRO	A	181	-0.362	58.734	39.152	1.00 98.39
ATOM	1394	CD	PRO	A	181	0.268	58.736	37.663	1.00 94.17
ATOM	1395	N	GLU	A	182	-3.567	57.456	38.141	1.00100.00
ATOM	1396	CA	GLU	A	182	-4.822	58.161	37.876	1.00 98.21
ATOM	1397	C	GLU	A	182	-5.359	58.856	39.154	1.00100.00
ATOM	1398	O	GLU	A	182	-6.404	59.497	39.167	1.00 99.44
ATOM	1399	CB	GLU	A	182	-5.854	57.142	37.356	1.00 98.57
ATOM	1400	CG	GLU	A	182	-5.880	57.077	35.816	1.00100.00
ATOM	1401	CD	GLU	A	182	-7.013	57.938	35.300	1.00100.00
ATOM	1402	OE1	GLU	A	182	-7.817	58.385	36.105	1.00100.00
ATOM	1403	OE2	GLU	A	182	-7.084	58.153	34.091	1.00100.00
ATOM	1404	N	ASP	A	183	-4.607	58.672	40.265	1.00 98.63
ATOM	1405	CA	ASP	A	183	-5.021	59.257	41.552	1.00 97.49
ATOM	1406	C	ASP	A	183	-4.126	60.472	41.932	1.00100.00
ATOM	1407	O	ASP	A	183	-3.464	61.061	41.079	1.00100.00
ATOM	1408	CB	ASP	A	183	-4.946	58.144	42.619	1.00 98.36
ATOM	1409	CG	ASP	A	183	-3.612	57.409	42.547	1.00100.00
ATOM	1410	OD1	ASP	A	183	-3.471	56.556	41.668	1.00100.00
ATOM	1411	OD2	ASP	A	183	-2.741	57.688	43.364	1.00100.00
ATOM	1412	N	PRO	A	184	-4.187	60.906	43.237	1.00 97.96
ATOM	1413	CA	PRO	A	184	-3.311	61.985	43.738	1.00 97.92
ATOM	1414	C	PRO	A	184	-1.865	61.528	44.071	1.00 97.89
ATOM	1415	O	PRO	A	184	-1.348	61.748	45.159	1.00100.00
ATOM	1416	CB	PRO	A	184	-3.973	62.561	44.992	1.00 98.86
ATOM	1417	CG	PRO	A	184	-5.262	61.777	45.284	1.00100.00
ATOM	1418	CD	PRO	A	184	-5.122	60.532	44.284	1.00 97.20
ATOM	1419	N	SER	A	185	-1.249	60.840	43.071	1.00 82.40
ATOM	1420	CA	SER	A	185	0.196	60.496	43.086	1.00 75.26
ATOM	1421	C	SER	A	185	0.748	60.563	41.623	1.00 71.84
ATOM	1422	O	SER	A	185	-0.006	60.525	40.670	1.00 77.97
ATOM	1423	CB	SER	A	185	0.337	59.068	43.636	1.00 73.41
ATOM	1424	OG	SER	A	185	0.672	59.109	45.027	1.00 63.60
ATOM	1425	N	ARG	A	186	2.107	60.704	41.461	1.00 57.89
ATOM	1426	CA	ARG	A	186	2.650	60.971	40.088	1.00 56.00
ATOM	1427	C	ARG	A	186	3.725	59.943	39.633	1.00 59.64
ATOM	1428	O	ARG	A	186	4.473	60.157	38.688	1.00 60.30
ATOM	1429	CB	ARG	A	186	3.258	62.393	40.064	1.00 63.74
ATOM	1430	CG	ARG	A	186	2.339	63.457	40.677	1.00 80.44
ATOM	1431	CD	ARG	A	186	1.188	63.874	39.736	1.00 71.31
ATOM	1432	NE	ARG	A	186	1.316	63.215	38.436	1.00 79.64
ATOM	1433	CZ	ARG	A	186	0.185	62.862	37.784	1.00 95.30
ATOM	1434	NH1	ARG	A	186	-0.999	63.109	38.312	1.00 56.25
ATOM	1435	NH2	ARG	A	186	0.276	62.232	36.603	1.00 89.98
ATOM	1436	N	LYS	A	187	3.892	58.778	40.265	1.00 54.50
ATOM	1437	CA	LYS	A	187	4.891	57.805	39.851	1.00 51.93
ATOM	1438	C	LYS	A	187	4.506	56.436	40.276	1.00 52.96
ATOM	1439	O	LYS	A	187	3.971	56.236	41.368	1.00 53.58
ATOM	1440	CB	LYS	A	187	6.247	58.047	40.470	1.00 53.78
ATOM	1441	CG	LYS	A	187	7.427	57.714	39.574	1.00 43.05

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ATOM   1442  CD  LYS A 187       8.517  58.761  39.762  1.00 53.36
ATOM   1443  CE  LYS A 187       9.870  58.468  39.146  1.00 39.68
ATOM   1444  NZ  LYS A 187      10.795  59.601  39.341  1.00 40.19
ATOM   1445  N   ILE A 188       4.819  55.502  39.403  1.00 46.36
ATOM   1446  CA  ILE A 188       4.565  54.128  39.700  1.00 43.57
ATOM   1447  C   ILE A 188       5.824  53.311  39.851  1.00 42.64
ATOM   1448  O   ILE A 188       6.647  53.189  38.937  1.00 41.55
ATOM   1449  CB  ILE A 188       3.579  53.425  38.826  1.00 45.64
ATOM   1450  CG1 ILE A 188       2.193  54.021  39.047  1.00 45.82
ATOM   1451  CG2 ILE A 188       3.590  51.969  39.273  1.00 43.43
ATOM   1452  CD1 ILE A 188       1.448  53.505  40.276  1.00 62.08
ATOM   1453  N   TYR A 189       5.950  52.757  41.042  1.00 35.58
ATOM   1454  CA  TYR A 189       7.079  51.933  41.356  1.00 37.57
ATOM   1455  C   TYR A 189       6.652  50.465  41.359  1.00 44.89
ATOM   1456  O   TYR A 189       5.656  50.092  41.999  1.00 44.33
ATOM   1457  CB  TYR A 189       7.752  52.392  42.661  1.00 37.85
ATOM   1458  CG  TYR A 189       8.692  53.563  42.456  1.00 34.49
ATOM   1459  CD1 TYR A 189       9.968  53.375  41.930  1.00 35.93
ATOM   1460  CD2 TYR A 189       8.310  54.859  42.813  1.00 32.44
ATOM   1461  CE1 TYR A 189      10.843  54.449  41.753  1.00 36.88
ATOM   1462  CE2 TYR A 189       9.170  55.945  42.647  1.00 31.63
ATOM   1463  CZ  TYR A 189      10.441  55.734  42.113  1.00 44.54
ATOM   1464  OH  TYR A 189      11.296  56.788  41.929  1.00 57.77
ATOM   1465  N   LYS A 190       7.413  49.651  40.608  1.00 42.91
ATOM   1466  CA  LYS A 190       7.173  48.210  40.420  1.00 42.22
ATOM   1467  C   LYS A 190       8.152  47.262  41.143  1.00 40.73
ATOM   1468  O   LYS A 190       9.398  47.400  41.093  1.00 35.69
ATOM   1469  CB  LYS A 190       7.007  47.839  38.944  1.00 45.87
ATOM   1470  CG  LYS A 190       5.735  48.403  38.306  1.00 71.08
ATOM   1471  CD  LYS A 190       5.758  48.384  36.779  1.00 84.62
ATOM   1472  CE  LYS A 190       4.386  48.157  36.147  1.00100.00
ATOM   1473  NZ  LYS A 190       4.299  46.930  35.329  1.00100.00
ATOM   1474  N   PHE A 191       7.539  46.264  41.812  1.00 35.01
ATOM   1475  CA  PHE A 191       8.276  45.304  42.592  1.00 31.57
ATOM   1476  C   PHE A 191       7.792  43.871  42.465  1.00 30.89
ATOM   1477  O   PHE A 191       6.603  43.584  42.377  1.00 25.06
ATOM   1478  CB  PHE A 191       8.217  45.734  44.080  1.00 32.11
ATOM   1479  CG  PHE A 191       8.570  47.190  44.372  1.00 29.24
ATOM   1480  CD1 PHE A 191       9.895  47.593  44.539  1.00 31.81
ATOM   1481  CD2 PHE A 191       7.565  48.147  44.508  1.00 30.17
ATOM   1482  CE1 PHE A 191      10.230  48.925  44.805  1.00 34.10
ATOM   1483  CE2 PHE A 191       7.866  49.483  44.776  1.00 33.69
ATOM   1484  CZ  PHE A 191       9.201  49.860  44.928  1.00 33.32
ATOM   1485  N   ILE A 192       8.764  42.961  42.505  1.00 35.75
ATOM   1486  CA  ILE A 192       8.525  41.520  42.415  1.00 37.02
ATOM   1487  C   ILE A 192       9.255  40.653  43.469  1.00 33.05
ATOM   1488  O   ILE A 192      10.489  40.672  43.593  1.00 30.73
ATOM   1489  CB  ILE A 192       8.850  40.970  41.025  1.00 42.45
ATOM   1490  CG1 ILE A 192       8.289  41.914  39.981  1.00 46.39
ATOM   1491  CG2 ILE A 192       8.251  39.567  40.859  1.00 44.02
ATOM   1492  CD1 ILE A 192       7.609  41.231  38.798  1.00 69.61
ATOM   1493  N   GLN A 193       8.459  39.864  44.195  1.00 27.51
ATOM   1494  CA  GLN A 193       8.954  38.908  45.177  1.00 32.05
ATOM   1495  C   GLN A 193       8.626  37.488  44.757  1.00 44.32
ATOM   1496  O   GLN A 193       7.583  36.926  45.120  1.00 43.11
ATOM   1497  CB  GLN A 193       8.502  39.100  46.638  1.00 33.44
ATOM   1498  CG  GLN A 193       9.285  38.203  47.632  1.00 22.34
ATOM   1499  CD  GLN A 193      10.824  38.337  47.636  1.00 48.52
ATOM   1500  OE1 GLN A 193      11.557  37.537  47.016  1.00 45.24
ATOM   1501  NE2 GLN A 193      11.326  39.330  48.373  1.00 24.82
ATOM   1502  N   LYS A 194       9.543  36.908  43.993  1.00 46.91
ATOM   1503  CA  LYS A 194       9.384  35.540  43.529  1.00 47.56
ATOM   1504  C   LYS A 194       9.456  34.524  44.666  1.00 49.56
ATOM   1505  O   LYS A 194       8.777  33.520  44.598  1.00 50.85
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ATOM   1506  CB  LYS A 194      10.385  35.159  42.439  1.00 48.11
ATOM   1507  CG  LYS A 194       9.884  35.443  41.031  1.00 55.70
ATOM   1508  CD  LYS A 194      10.895  36.200  40.179  1.00 67.67
ATOM   1509  CE  LYS A 194      10.614  36.122  38.682  1.00 81.92
ATOM   1510  NZ  LYS A 194      11.284  37.185  37.910  1.00 88.34
ATOM   1511  N   VAL A 195      10.308  34.753  45.689  1.00 39.55
ATOM   1512  CA  VAL A 195      10.422  33.780  46.764  1.00 33.56
ATOM   1513  C   VAL A 195       9.261  33.862  47.698  1.00 35.67
ATOM   1514  O   VAL A 195       8.804  34.945  48.034  1.00 38.69
ATOM   1515  CB  VAL A 195      11.716  33.844  47.560  1.00 32.62
ATOM   1516  CG1 VAL A 195      11.849  32.539  48.310  1.00 32.40
ATOM   1517  CG2 VAL A 195      12.933  34.029  46.667  1.00 30.55
ATOM   1518  N   PRO A 196       8.770  32.717  48.126  1.00 27.75
ATOM   1519  CA  PRO A 196       7.653  32.757  49.038  1.00 26.18
ATOM   1520  C   PRO A 196       8.132  33.236  50.410  1.00 35.86
ATOM   1521  O   PRO A 196       9.185  32.809  50.899  1.00 35.43
ATOM   1522  CB  PRO A 196       7.022  31.359  49.044  1.00 26.04
ATOM   1523  CG  PRO A 196       7.856  30.472  48.113  1.00 27.79
ATOM   1524  CD  PRO A 196       8.964  31.352  47.546  1.00 25.40
ATOM   1525  N   ILE A 197       7.388  34.171  51.009  1.00 29.92
ATOM   1526  CA  ILE A 197       7.772  34.697  52.284  1.00 26.98
ATOM   1527  C   ILE A 197       6.544  34.809  53.128  1.00 34.88
ATOM   1528  O   ILE A 197       5.444  34.788  52.606  1.00 29.68
ATOM   1529  CB  ILE A 197       8.334  36.100  52.094  1.00 27.90
ATOM   1530  CG1 ILE A 197       7.342  36.867  51.254  1.00 27.78
ATOM   1531  CG2 ILE A 197       9.659  36.091  51.337  1.00 28.12
ATOM   1532  CD1 ILE A 197       7.494  38.378  51.438  1.00 19.03
ATOM   1533  N   PRO A 198       6.743  34.936  54.447  1.00 36.02
ATOM   1534  CA  PRO A 198       5.647  35.110  55.410  1.00 31.31
ATOM   1535  C   PRO A 198       5.299  36.583  55.308  1.00 28.27
ATOM   1536  O   PRO A 198       6.212  37.391  55.115  1.00 22.70
ATOM   1537  CB  PRO A 198       6.252  34.849  56.794  1.00 31.17
ATOM   1538  CG  PRO A 198       7.768  34.768  56.615  1.00 34.94
ATOM   1539  CD  PRO A 198       8.057  34.706  55.122  1.00 32.99
ATOM   1540  N   CYS A 199       4.011  36.939  55.405  1.00 27.60
ATOM   1541  CA  CYS A 199       3.555  38.360  55.289  1.00 27.66
ATOM   1542  C   CYS A 199       4.255  39.390  56.187  1.00 30.13
ATOM   1543  O   CYS A 199       4.294  40.596  55.895  1.00 29.50
ATOM   1544  CB  CYS A 199       2.025  38.534  55.242  1.00 27.18
ATOM   1545  SG  CYS A 199       1.232  38.279  56.841  1.00 30.85
ATOM   1546  N   TYR A 200       4.847  38.903  57.270  1.00 26.15
ATOM   1547  CA  TYR A 200       5.538  39.798  58.123  1.00 28.28
ATOM   1548  C   TYR A 200       6.760  40.395  57.483  1.00 32.29
ATOM   1549  O   TYR A 200       7.359  41.286  58.036  1.00 31.56
ATOM   1550  CB  TYR A 200       5.844  39.215  59.489  1.00 30.59
ATOM   1551  CG  TYR A 200       6.989  38.272  59.568  1.00 28.28
ATOM   1552  CD1 TYR A 200       8.288  38.733  59.689  1.00 29.48
ATOM   1553  CD2 TYR A 200       6.756  36.903  59.475  1.00 27.55
ATOM   1554  CE1 TYR A 200       9.377  37.862  59.825  1.00 21.42
ATOM   1555  CE2 TYR A 200       7.838  36.015  59.595  1.00 27.41
ATOM   1556  CZ  TYR A 200       9.144  36.488  59.737  1.00 25.11
ATOM   1557  OH  TYR A 200      10.215  35.614  59.880  1.00 27.62
ATOM   1558  N   LEU A 201       7.113  39.897  56.313  1.00 31.66
ATOM   1559  CA  LEU A 201       8.278  40.378  55.579  1.00 29.49
ATOM   1560  C   LEU A 201       7.914  41.343  54.484  1.00 33.65
ATOM   1561  O   LEU A 201       8.767  41.737  53.686  1.00 35.31
ATOM   1562  CB  LEU A 201       9.225  39.275  55.035  1.00 27.04
ATOM   1563  CG  LEU A 201       9.697  38.271  56.071  1.00 27.42
ATOM   1564  CD1 LEU A 201      10.254  37.030  55.390  1.00 23.71
ATOM   1565  CD2 LEU A 201      10.764  38.913  56.957  1.00 30.55
ATOM   1566  N   ILE A 202       6.648  41.710  54.438  1.00 28.66
ATOM   1567  CA  ILE A 202       6.249  42.674  53.433  1.00 29.57
ATOM   1568  C   ILE A 202       6.636  44.074  53.951  1.00 40.28
ATOM   1569  O   ILE A 202       6.192  44.493  55.027  1.00 40.75
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ATOM	1570	CB	ILE	A	202	4.733	42.651	53.182	1.00 31.18
ATOM	1571	CG1	ILE	A	202	4.250	41.429	52.405	1.00 28.21
ATOM	1572	CG2	ILE	A	202	4.259	43.962	52.521	1.00 29.23
ATOM	1573	CD1	ILE	A	202	2.724	41.288	52.449	1.00 23.01
ATOM	1574	N	ALA	A	203	7.445	44.813	53.197	1.00 39.14
ATOM	1575	CA	ALA	A	203	7.840	46.150	53.611	1.00 37.03
ATOM	1576	C	ALA	A	203	7.819	47.159	52.482	1.00 34.32
ATOM	1577	O	ALA	A	203	8.060	46.836	51.311	1.00 30.63
ATOM	1578	CB	ALA	A	203	9.180	46.143	54.309	1.00 38.22
ATOM	1579	N	LEU	A	204	7.514	48.388	52.910	1.00 33.64
ATOM	1580	CA	LEU	A	204	7.388	49.604	52.102	1.00 32.56
ATOM	1581	C	LEU	A	204	7.993	50.817	52.812	1.00 37.69
ATOM	1582	O	LEU	A	204	7.854	51.037	54.034	1.00 32.66
ATOM	1583	CB	LEU	A	204	5.906	49.929	51.718	1.00 29.74
ATOM	1584	CG	LEU	A	204	5.706	51.182	50.855	1.00 29.64
ATOM	1585	CD1	LEU	A	204	6.263	50.994	49.445	1.00 29.47
ATOM	1586	CD2	LEU	A	204	4.222	51.515	50.750	1.00 33.50
ATOM	1587	N	VAL	A	205	8.670	51.603	51.991	1.00 36.87
ATOM	1588	CA	VAL	A	205	9.305	52.821	52.415	1.00 35.15
ATOM	1589	C	VAL	A	205	9.224	53.795	51.284	1.00 38.41
ATOM	1590	O	VAL	A	205	9.575	53.462	50.148	1.00 39.50
ATOM	1591	CB	VAL	A	205	10.769	52.651	52.804	1.00 36.06
ATOM	1592	CG1	VAL	A	205	11.466	51.794	51.757	1.00 35.08
ATOM	1593	CG2	VAL	A	205	11.432	54.020	52.833	1.00 35.98
ATOM	1594	N	VAL	A	206	8.750	54.983	51.623	1.00 33.54
ATOM	1595	CA	VAL	A	206	8.623	56.104	50.687	1.00 31.81
ATOM	1596	C	VAL	A	206	9.300	57.343	51.249	1.00 31.62
ATOM	1597	O	VAL	A	206	9.076	57.722	52.406	1.00 34.81
ATOM	1598	CB	VAL	A	206	7.179	56.405	50.305	1.00 33.35
ATOM	1599	CG1	VAL	A	206	7.129	57.243	49.029	1.00 33.44
ATOM	1600	CG2	VAL	A	206	6.452	55.084	50.109	1.00 31.98
ATOM	1601	N	GLY	A	207	10.130	57.959	50.431	1.00 24.94
ATOM	1602	CA	GLY	A	207	10.807	59.168	50.861	1.00 27.25
ATOM	1603	C	GLY	A	207	11.802	59.632	49.838	1.00 38.81
ATOM	1604	O	GLY	A	207	12.046	58.966	48.840	1.00 39.82
ATOM	1605	N	ALA	A	208	12.375	60.783	50.113	1.00 41.07
ATOM	1606	CA	ALA	A	208	13.370	61.354	49.233	1.00 42.72
ATOM	1607	C	ALA	A	208	14.660	60.550	49.356	1.00 49.10
ATOM	1608	O	ALA	A	208	15.651	60.997	49.957	1.00 51.30
ATOM	1609	CB	ALA	A	208	13.605	62.810	49.589	1.00 42.95
ATOM	1610	N	LEU	A	209	14.623	59.350	48.773	1.00 40.92
ATOM	1611	CA	LEU	A	209	15.739	58.440	48.825	1.00 39.55
ATOM	1612	C	LEU	A	209	16.756	58.575	47.743	1.00 47.96
ATOM	1613	O	LEU	A	209	16.420	58.843	46.597	1.00 49.44
ATOM	1614	CB	LEU	A	209	15.269	56.994	48.894	1.00 37.97
ATOM	1615	CG	LEU	A	209	14.420	56.803	50.129	1.00 40.46
ATOM	1616	CD1	LEU	A	209	13.713	55.469	50.075	1.00 36.99
ATOM	1617	CD2	LEU	A	209	15.283	56.921	51.387	1.00 43.31
ATOM	1618	N	GLU	A	210	17.999	58.317	48.182	1.00 42.68
ATOM	1619	CA	GLU	A	210	19.205	58.311	47.381	1.00 40.30
ATOM	1620	C	GLU	A	210	19.965	57.056	47.693	1.00 47.51
ATOM	1621	O	GLU	A	210	19.708	56.432	48.721	1.00 47.89
ATOM	1622	CB	GLU	A	210	20.084	59.553	47.613	1.00 42.01
ATOM	1623	CG	GLU	A	210	19.699	60.734	46.697	1.00 58.26
ATOM	1624	CD	GLU	A	210	20.524	61.970	46.897	1.00100.00
ATOM	1625	OE1	GLU	A	210	21.629	61.968	47.451	1.00 95.26
ATOM	1626	OE2	GLU	A	210	19.935	63.047	46.486	1.00100.00
ATOM	1627	N	SER	A	211	20.895	56.662	46.805	1.00 45.01
ATOM	1628	CA	SER	A	211	21.661	55.442	47.013	1.00 42.25
ATOM	1629	C	SER	A	211	23.143	55.535	46.667	1.00 43.37
ATOM	1630	O	SER	A	211	23.649	56.493	46.086	1.00 46.43
ATOM	1631	CB	SER	A	211	21.025	54.233	46.346	1.00 44.33
ATOM	1632	OG	SER	A	211	21.274	54.244	44.934	1.00 54.15
ATOM	1633	N	ARG	A	212	23.829	54.497	47.053	1.00 34.85

ATOM	1634	CA	ARG	A	212	25.229	54.328	46.791	1.00 35.41
ATOM	1635	C	ARG	A	212	25.430	52.838	46.567	1.00 45.39
ATOM	1636	O	ARG	A	212	24.840	52.027	47.276	1.00 48.85
ATOM	1637	CB	ARG	A	212	26.101	54.846	47.915	1.00 37.25
ATOM	1638	CG	ARG	A	212	27.151	55.827	47.402	1.00 68.10
ATOM	1639	CD	ARG	A	212	26.532	56.962	46.587	1.00 76.55
ATOM	1640	NE	ARG	A	212	26.695	58.307	47.148	1.00 55.19
ATOM	1641	CZ	ARG	A	212	25.845	59.301	46.867	1.00 70.87
ATOM	1642	NH1	ARG	A	212	24.806	59.105	46.059	1.00 35.71
ATOM	1643	NH2	ARG	A	212	26.032	60.516	47.392	1.00 73.35
ATOM	1644	N	GLN	A	213	26.210	52.442	45.567	1.00 40.74
ATOM	1645	CA	GLN	A	213	26.408	51.021	45.331	1.00 39.90
ATOM	1646	C	GLN	A	213	27.646	50.537	46.050	1.00 46.34
ATOM	1647	O	GLN	A	213	28.740	50.981	45.741	1.00 53.77
ATOM	1648	CB	GLN	A	213	26.545	50.741	43.846	1.00 40.99
ATOM	1649	CG	GLN	A	213	26.976	49.296	43.532	1.00 55.79
ATOM	1650	CD	GLN	A	213	26.292	48.743	42.301	1.00 76.04
ATOM	1651	OE1	GLN	A	213	26.275	47.523	42.102	1.00 86.66
ATOM	1652	NE2	GLN	A	213	25.700	49.618	41.489	1.00 55.45
ATOM	1653	N	ILE	A	214	27.495	49.649	47.013	1.00 33.12
ATOM	1654	CA	ILE	A	214	28.663	49.206	47.743	1.00 32.55
ATOM	1655	C	ILE	A	214	28.911	47.765	47.536	1.00 39.29
ATOM	1656	O	ILE	A	214	29.726	47.162	48.230	1.00 42.41
ATOM	1657	CB	ILE	A	214	28.546	49.428	49.250	1.00 35.72
ATOM	1658	CG1	ILE	A	214	27.395	48.573	49.791	1.00 36.13
ATOM	1659	CG2	ILE	A	214	28.344	50.911	49.598	1.00 35.79
ATOM	1660	CD1	ILE	A	214	27.067	48.841	51.260	1.00 46.69
ATOM	1661	N	GLY	A	215	28.199	47.197	46.598	1.00 35.02
ATOM	1662	CA	GLY	A	215	28.638	45.855	46.234	1.00 34.88
ATOM	1663	C	GLY	A	215	27.970	45.405	44.950	1.00 41.09
ATOM	1664	O	GLY	A	215	27.083	46.048	44.425	1.00 44.25
ATOM	1665	N	PRO	A	216	28.448	44.262	44.410	1.00 39.62
ATOM	1666	CA	PRO	A	216	27.890	43.720	43.197	1.00 39.69
ATOM	1667	C	PRO	A	216	26.369	43.661	43.253	1.00 41.56
ATOM	1668	O	PRO	A	216	25.655	43.817	42.240	1.00 44.35
ATOM	1669	CB	PRO	A	216	28.448	42.311	42.996	1.00 39.91
ATOM	1670	CG	PRO	A	216	29.377	41.993	44.164	1.00 41.54
ATOM	1671	CD	PRO	A	216	29.514	43.411	44.897	1.00 37.70
ATOM	1672	N	ARG	A	217	25.846	43.398	44.477	1.00 31.04
ATOM	1673	CA	ARG	A	217	24.421	43.328	44.652	1.00 29.22
ATOM	1674	C	ARG	A	217	23.928	44.109	45.872	1.00 38.24
ATOM	1675	O	ARG	A	217	22.861	43.885	46.368	1.00 40.69
ATOM	1676	CB	ARG	A	217	24.012	41.844	44.790	1.00 22.75
ATOM	1677	CG	ARG	A	217	25.221	40.963	45.109	1.00 40.77
ATOM	1678	CD	ARG	A	217	24.828	39.774	45.985	1.00 34.08
ATOM	1679	NE	ARG	A	217	26.020	39.183	46.581	1.00 45.20
ATOM	1680	CZ	ARG	A	217	25.955	37.894	46.911	1.00 65.13
ATOM	1681	NH1	ARG	A	217	24.832	37.220	46.716	1.00 42.40
ATOM	1682	NH2	ARG	A	217	26.997	37.300	47.472	1.00 48.08
ATOM	1683	N	THR	A	218	24.784	45.022	46.404	1.00 31.00
ATOM	1684	CA	THR	A	218	24.309	45.886	47.487	1.00 31.00
ATOM	1685	C	THR	A	218	24.128	47.319	47.021	1.00 43.60
ATOM	1686	O	THR	A	218	25.065	47.930	46.512	1.00 48.42
ATOM	1687	CB	THR	A	218	25.315	45.845	48.640	1.00 36.95
ATOM	1688	OG1	THR	A	218	25.430	44.517	49.139	1.00 45.66
ATOM	1689	CG2	THR	A	218	24.826	46.751	49.766	1.00 34.17
ATOM	1690	N	LEU	A	219	23.099	48.018	47.431	1.00 39.19
ATOM	1691	CA	LEU	A	219	23.055	49.452	47.315	1.00 38.18
ATOM	1692	C	LEU	A	219	22.713	50.000	48.695	1.00 42.32
ATOM	1693	O	LEU	A	219	22.108	49.289	49.498	1.00 43.67
ATOM	1694	CB	LEU	A	219	21.927	49.841	46.356	1.00 37.05
ATOM	1695	CG	LEU	A	219	22.386	50.657	45.168	1.00 39.31
ATOM	1696	CD1	LEU	A	219	23.670	50.064	44.613	1.00 40.57
ATOM	1697	CD2	LEU	A	219	21.283	50.619	44.131	1.00 29.39

ATOM	1698	N	VAL	A	220	23.066	51.241	48.976	1.00 35.01
ATOM	1699	CA	VAL	A	220	22.741	51.830	50.253	1.00 36.98
ATOM	1700	C	VAL	A	220	21.736	52.923	50.043	1.00 44.08
ATOM	1701	O	VAL	A	220	21.959	53.835	49.256	1.00 46.60
ATOM	1702	CB	VAL	A	220	23.965	52.346	51.028	1.00 44.95
ATOM	1703	CG1	VAL	A	220	23.675	52.428	52.516	1.00 43.16
ATOM	1704	CG2	VAL	A	220	25.138	51.382	50.828	1.00 47.70
ATOM	1705	N	TRP	A	221	20.622	52.818	50.731	1.00 41.98
ATOM	1706	CA	TRP	A	221	19.605	53.828	50.602	1.00 41.64
ATOM	1707	C	TRP	A	221	19.464	54.612	51.872	1.00 42.40
ATOM	1708	O	TRP	A	221	19.461	54.060	52.960	1.00 45.56
ATOM	1709	CB	TRP	A	221	18.256	53.245	50.186	1.00 41.24
ATOM	1710	CG	TRP	A	221	18.353	52.459	48.918	1.00 42.59
ATOM	1711	CD1	TRP	A	221	18.888	51.225	48.793	1.00 45.35
ATOM	1712	CD2	TRP	A	221	17.949	52.873	47.590	1.00 41.62
ATOM	1713	NE1	TRP	A	221	18.826	50.832	47.478	1.00 44.74
ATOM	1714	CE2	TRP	A	221	18.243	51.821	46.720	1.00 45.31
ATOM	1715	CE3	TRP	A	221	17.345	54.009	47.061	1.00 41.17
ATOM	1716	CZ2	TRP	A	221	17.958	51.902	45.346	1.00 42.60
ATOM	1717	CZ3	TRP	A	221	17.054	54.083	45.710	1.00 39.08
ATOM	1718	CH2	TRP	A	221	17.360	53.040	44.864	1.00 38.48
ATOM	1719	N	SER	A	222	19.271	55.896	51.688	1.00 37.01
ATOM	1720	CA	SER	A	222	19.017	56.846	52.748	1.00 38.05
ATOM	1721	C	SER	A	222	18.853	58.251	52.205	1.00 45.28
ATOM	1722	O	SER	A	222	19.005	58.503	51.008	1.00 44.02
ATOM	1723	CB	SER	A	222	20.098	56.816	53.820	1.00 39.07
ATOM	1724	OG	SER	A	222	21.322	57.149	53.229	1.00 42.36
ATOM	1725	N	GLU	A	223	18.586	59.190	53.088	1.00 40.91
ATOM	1726	CA	GLU	A	223	18.465	60.527	52.584	1.00 41.97
ATOM	1727	C	GLU	A	223	19.843	61.042	52.234	1.00 50.17
ATOM	1728	O	GLU	A	223	20.829	60.701	52.863	1.00 52.02
ATOM	1729	CB	GLU	A	223	17.856	61.483	53.597	1.00 43.06
ATOM	1730	CG	GLU	A	223	16.364	61.262	53.861	1.00 51.71
ATOM	1731	CD	GLU	A	223	15.799	62.478	54.545	1.00 84.51
ATOM	1732	OE1	GLU	A	223	15.905	63.610	54.085	1.00 56.82
ATOM	1733	OE2	GLU	A	223	15.244	62.222	55.705	1.00 88.87
ATOM	1734	N	LYS	A	224	19.892	61.875	51.229	1.00 47.39
ATOM	1735	CA	LYS	A	224	21.139	62.456	50.792	1.00 48.51
ATOM	1736	C	LYS	A	224	22.163	62.683	51.930	1.00 50.90
ATOM	1737	O	LYS	A	224	23.382	62.569	51.736	1.00 51.55
ATOM	1738	CB	LYS	A	224	20.843	63.736	49.986	1.00 51.58
ATOM	1739	CG	LYS	A	224	22.039	64.648	49.723	1.00 81.16
ATOM	1740	CD	LYS	A	224	21.954	65.397	48.392	1.00 97.82
ATOM	1741	CE	LYS	A	224	21.646	66.891	48.530	1.00100.00
ATOM	1742	NZ	LYS	A	224	22.056	67.700	47.362	1.00100.00
ATOM	1743	N	GLU	A	225	21.683	63.011	53.123	1.00 45.77
ATOM	1744	CA	GLU	A	225	22.607	63.309	54.199	1.00 46.00
ATOM	1745	C	GLU	A	225	23.227	62.150	54.902	1.00 47.99
ATOM	1746	O	GLU	A	225	24.107	62.354	55.732	1.00 47.21
ATOM	1747	CB	GLU	A	225	22.057	64.296	55.210	1.00 47.71
ATOM	1748	CG	GLU	A	225	20.530	64.296	55.182	1.00 63.24
ATOM	1749	CD	GLU	A	225	19.931	65.219	54.150	1.00 75.13
ATOM	1750	OE1	GLU	A	225	20.187	66.420	54.046	1.00 54.64
ATOM	1751	OE2	GLU	A	225	19.039	64.578	53.420	1.00 49.64
ATOM	1752	N	GLN	A	226	22.798	60.949	54.564	1.00 43.92
ATOM	1753	CA	GLN	A	226	23.340	59.772	55.224	1.00 43.91
ATOM	1754	C	GLN	A	226	24.036	58.756	54.322	1.00 45.86
ATOM	1755	O	GLN	A	226	24.756	57.871	54.806	1.00 45.70
ATOM	1756	CB	GLN	A	226	22.252	59.084	56.063	1.00 45.27
ATOM	1757	CG	GLN	A	226	21.965	59.790	57.400	1.00 31.17
ATOM	1758	CD	GLN	A	226	21.297	61.155	57.302	1.00 44.48
ATOM	1759	OE1	GLN	A	226	21.823	62.149	57.820	1.00 37.36
ATOM	1760	NE2	GLN	A	226	20.115	61.202	56.696	1.00 30.28
ATOM	1761	N	VAL	A	227	23.814	58.871	53.021	1.00 41.20

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ATOM   1762  CA  VAL A 227      24.406  57.947  52.071  1.00 43.13
ATOM   1763  C   VAL A 227      25.884  57.670  52.261  1.00 50.55
ATOM   1764  O   VAL A 227      26.298  56.518  52.480  1.00 53.01
ATOM   1765  CB  VAL A 227      24.155  58.293  50.604  1.00 49.39
ATOM   1766  CG1 VAL A 227      24.319  57.029  49.771  1.00 48.89
ATOM   1767  CG2 VAL A 227      22.752  58.851  50.421  1.00 50.47
ATOM   1768  N   GLU A 228      26.696  58.718  52.170  1.00 44.08
ATOM   1769  CA  GLU A 228      28.123  58.542  52.310  1.00 41.71
ATOM   1770  C   GLU A 228      28.514  57.871  53.583  1.00 44.20
ATOM   1771  O   GLU A 228      29.227  56.868  53.589  1.00 44.88
ATOM   1772  CB  GLU A 228      28.935  59.824  52.102  1.00 43.08
ATOM   1773  CG  GLU A 228      29.153  60.161  50.611  1.00 64.74
ATOM   1774  CD  GLU A 228      29.114  58.965  49.701  1.00 84.29
ATOM   1775  OE1 GLU A 228      29.975  58.107  49.685  1.00 84.36
ATOM   1776  OE2 GLU A 228      28.064  58.951  48.917  1.00 73.81
ATOM   1777  N   LYS A 229      28.066  58.423  54.685  1.00 39.79
ATOM   1778  CA  LYS A 229      28.449  57.796  55.922  1.00 39.04
ATOM   1779  C   LYS A 229      27.949  56.375  55.930  1.00 40.38
ATOM   1780  O   LYS A 229      28.639  55.433  56.346  1.00 43.63
ATOM   1781  CB  LYS A 229      28.129  58.585  57.187  1.00 39.79
ATOM   1782  CG  LYS A 229      28.903  58.072  58.394  1.00 63.75
ATOM   1783  CD  LYS A 229      28.498  58.763  59.685  1.00 77.46
ATOM   1784  CE  LYS A 229      29.677  59.084  60.593  1.00 94.73
ATOM   1785  NZ  LYS A 229      30.344  60.353  60.256  1.00100.00
ATOM   1786  N   SER A 230      26.741  56.220  55.428  1.00 28.48
ATOM   1787  CA  SER A 230      26.174  54.891  55.377  1.00 25.93
ATOM   1788  C   SER A 230      27.089  53.988  54.587  1.00 30.26
ATOM   1789  O   SER A 230      27.469  52.855  54.955  1.00 28.48
ATOM   1790  CB  SER A 230      24.824  54.927  54.694  1.00 30.08
ATOM   1791  OG  SER A 230      23.822  55.293  55.605  1.00 41.60
ATOM   1792  N   ALA A 231      27.436  54.536  53.459  1.00 31.13
ATOM   1793  CA  ALA A 231      28.288  53.820  52.593  1.00 36.66
ATOM   1794  C   ALA A 231      29.597  53.383  53.270  1.00 47.68
ATOM   1795  O   ALA A 231      30.003  52.238  53.103  1.00 54.59
ATOM   1796  CB  ALA A 231      28.406  54.518  51.257  1.00 38.49
ATOM   1797  N   TYR A 232      30.256  54.246  54.060  1.00 40.77
ATOM   1798  CA  TYR A 232      31.500  53.830  54.730  1.00 38.40
ATOM   1799  C   TYR A 232      31.265  52.721  55.753  1.00 39.70
ATOM   1800  O   TYR A 232      32.041  51.772  55.862  1.00 36.46
ATOM   1801  CB  TYR A 232      32.311  54.981  55.414  1.00 38.27
ATOM   1802  CG  TYR A 232      33.497  54.525  56.303  1.00 42.36
ATOM   1803  CD1 TYR A 232      34.755  54.238  55.753  1.00 46.41
ATOM   1804  CD2 TYR A 232      33.373  54.394  57.691  1.00 40.99
ATOM   1805  CE1 TYR A 232      35.835  53.815  56.534  1.00 47.23
ATOM   1806  CE2 TYR A 232      34.441  53.979  58.496  1.00 40.10
ATOM   1807  CZ  TYR A 232      35.680  53.695  57.916  1.00 48.59
ATOM   1808  OH  TYR A 232      36.734  53.282  58.698  1.00 51.92
ATOM   1809  N   GLU A 233      30.191  52.883  56.519  1.00 35.75
ATOM   1810  CA  GLU A 233      29.835  51.984  57.606  1.00 34.55
ATOM   1811  C   GLU A 233      29.633  50.498  57.252  1.00 38.39
ATOM   1812  O   GLU A 233      30.152  49.576  57.892  1.00 38.55
ATOM   1813  CB  GLU A 233      28.673  52.623  58.414  1.00 34.48
ATOM   1814  CG  GLU A 233      28.666  52.262  59.912  1.00 24.95
ATOM   1815  CD  GLU A 233      29.463  53.183  60.787  1.00 37.55
ATOM   1816  OE1 GLU A 233      29.408  54.410  60.741  1.00 55.33
ATOM   1817  OE2 GLU A 233      30.216  52.518  61.619  1.00 40.65
ATOM   1818  N   PHE A 234      28.867  50.282  56.202  1.00 33.02
ATOM   1819  CA  PHE A 234      28.493  48.974  55.719  1.00 29.90
ATOM   1820  C   PHE A 234      29.341  48.398  54.592  1.00 34.69
ATOM   1821  O   PHE A 234      28.883  47.521  53.823  1.00 34.21
ATOM   1822  CB  PHE A 234      27.020  49.081  55.293  1.00 30.23
ATOM   1823  CG  PHE A 234      26.215  49.752  56.394  1.00 30.32
ATOM   1824  CD1 PHE A 234      26.518  49.521  57.739  1.00 31.50
ATOM   1825  CD2 PHE A 234      25.151  50.605  56.102  1.00 28.66
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ATOM   1826  CE1 PHE A 234      25.780  50.103  58.772  1.00 30.43
ATOM   1827  CE2 PHE A 234      24.407  51.203  57.121  1.00 29.60
ATOM   1828  CZ  PHE A 234      24.725  50.959  58.458  1.00 27.47
ATOM   1829  N   SER A 235      30.571  48.874  54.476  1.00 29.55
ATOM   1830  CA  SER A 235      31.428  48.366  53.412  1.00 28.64
ATOM   1831  C   SER A 235      31.387  46.858  53.338  1.00 30.38
ATOM   1832  O   SER A 235      31.166  46.252  52.282  1.00 32.37
ATOM   1833  CB  SER A 235      32.861  48.787  53.604  1.00 31.15
ATOM   1834  OG  SER A 235      33.028  49.368  54.873  1.00 39.32
ATOM   1835  N   GLU A 236      31.698  46.299  54.504  1.00 22.49
ATOM   1836  CA  GLU A 236      31.815  44.873  54.737  1.00 23.79
ATOM   1837  C   GLU A 236      30.627  43.992  54.380  1.00 32.37
ATOM   1838  O   GLU A 236      30.697  42.772  54.545  1.00 29.91
ATOM   1839  CB  GLU A 236      32.305  44.529  56.134  1.00 24.06
ATOM   1840  CG  GLU A 236      33.491  45.403  56.585  1.00 22.96
ATOM   1841  CD  GLU A 236      33.600  45.492  58.090  1.00 66.18
ATOM   1842  OE1 GLU A 236      32.633  45.482  58.849  1.00 37.01
ATOM   1843  OE2 GLU A 236      34.848  45.518  58.494  1.00 78.68
ATOM   1844  N   THR A 237      29.560  44.593  53.891  1.00 34.11
ATOM   1845  CA  THR A 237      28.384  43.823  53.539  1.00 33.69
ATOM   1846  C   THR A 237      28.644  42.609  52.644  1.00 33.33
ATOM   1847  O   THR A 237      28.517  41.451  53.048  1.00 31.09
ATOM   1848  CB  THR A 237      27.218  44.710  53.057  1.00 37.99
ATOM   1849  OG1 THR A 237      26.899  45.675  54.048  1.00 33.49
ATOM   1850  CG2 THR A 237      25.995  43.862  52.744  1.00 25.66
ATOM   1851  N   GLU A 238      29.020  42.854  51.409  1.00 29.69
ATOM   1852  CA  GLU A 238      29.267  41.734  50.520  1.00 27.05
ATOM   1853  C   GLU A 238      30.071  40.638  51.146  1.00 33.17
ATOM   1854  O   GLU A 238      29.660  39.497  51.055  1.00 38.50
ATOM   1855  CB  GLU A 238      29.851  42.080  49.161  1.00 27.50
ATOM   1856  CG  GLU A 238      30.116  40.813  48.320  1.00 18.83
ATOM   1857  CD  GLU A 238      28.902  40.297  47.596  1.00 41.67
ATOM   1858  OE1 GLU A 238      27.848  40.909  47.464  1.00 33.59
ATOM   1859  OE2 GLU A 238      29.085  39.089  47.138  1.00 46.30
ATOM   1860  N   SER A 239      31.203  40.973  51.772  1.00 24.44
ATOM   1861  CA  SER A 239      32.045  39.957  52.387  1.00 24.60
ATOM   1862  C   SER A 239      31.245  39.060  53.344  1.00 35.72
ATOM   1863  O   SER A 239      31.379  37.830  53.360  1.00 35.25
ATOM   1864  CB  SER A 239      33.231  40.601  53.074  1.00 29.14
ATOM   1865  OG  SER A 239      32.747  41.590  53.961  1.00 54.60
ATOM   1866  N   MET A 240      30.382  39.703  54.154  1.00 33.13
ATOM   1867  CA  MET A 240      29.529  38.993  55.091  1.00 28.55
ATOM   1868  C   MET A 240      28.603  38.075  54.325  1.00 35.65
ATOM   1869  O   MET A 240      28.435  36.926  54.689  1.00 35.99
ATOM   1870  CB  MET A 240      28.736  39.945  55.993  1.00 26.50
ATOM   1871  CG  MET A 240      29.691  40.675  56.910  1.00 27.57
ATOM   1872  SD  MET A 240      28.871  41.986  57.833  1.00 32.91
ATOM   1873  CE  MET A 240      30.040  42.085  59.183  1.00 28.47
ATOM   1874  N   LEU A 241      28.019  38.603  53.243  1.00 32.77
ATOM   1875  CA  LEU A 241      27.120  37.859  52.381  1.00 29.87
ATOM   1876  C   LEU A 241      27.848  36.615  51.878  1.00 36.76
ATOM   1877  O   LEU A 241      27.302  35.509  51.858  1.00 36.97
ATOM   1878  CB  LEU A 241      26.715  38.753  51.196  1.00 29.71
ATOM   1879  CG  LEU A 241      25.283  39.289  51.237  1.00 37.68
ATOM   1880  CD1 LEU A 241      25.174  40.552  50.389  1.00 35.76
ATOM   1881  CD2 LEU A 241      24.309  38.257  50.673  1.00 45.60
ATOM   1882  N   LYS A 242      29.114  36.806  51.468  1.00 34.76
ATOM   1883  CA  LYS A 242      29.908  35.702  50.972  1.00 33.62
ATOM   1884  C   LYS A 242      30.072  34.690  52.039  1.00 32.18
ATOM   1885  O   LYS A 242      29.887  33.512  51.795  1.00 32.56
ATOM   1886  CB  LYS A 242      31.292  36.069  50.468  1.00 38.43
ATOM   1887  CG  LYS A 242      31.406  36.263  48.961  1.00 49.23
ATOM   1888  CD  LYS A 242      31.160  37.721  48.536  1.00 88.36
ATOM   1889  CE  LYS A 242      32.371  38.456  47.943  1.00100.00
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ATOM	1890	NZ	LYS	A	242	32.033	39.411	46.862	1.00100.00
ATOM	1891	N	ILE	A	243	30.428	35.154	53.227	1.00 30.87
ATOM	1892	CA	ILE	A	243	30.627	34.229	54.359	1.00 31.70
ATOM	1893	C	ILE	A	243	29.381	33.458	54.764	1.00 36.50
ATOM	1894	O	ILE	A	243	29.458	32.303	55.119	1.00 39.33
ATOM	1895	CB	ILE	A	243	31.227	34.886	55.579	1.00 32.36
ATOM	1896	CG1	ILE	A	243	32.630	35.337	55.222	1.00 32.09
ATOM	1897	CG2	ILE	A	243	31.243	33.891	56.718	1.00 28.26
ATOM	1898	CD1	ILE	A	243	33.035	36.578	55.981	1.00 20.09
ATOM	1899	N	ALA	A	244	28.237	34.120	54.708	1.00 32.10
ATOM	1900	CA	ALA	A	244	26.968	33.519	55.066	1.00 32.95
ATOM	1901	C	ALA	A	244	26.600	32.392	54.127	1.00 36.35
ATOM	1902	O	ALA	A	244	26.074	31.358	54.546	1.00 36.88
ATOM	1903	CB	ALA	A	244	25.858	34.576	55.123	1.00 34.02
ATOM	1904	N	GLU	A	245	26.890	32.617	52.846	1.00 31.20
ATOM	1905	CA	GLU	A	245	26.614	31.635	51.818	1.00 29.26
ATOM	1906	C	GLU	A	245	27.360	30.354	52.092	1.00 35.18
ATOM	1907	O	GLU	A	245	26.849	29.276	51.800	1.00 36.21
ATOM	1908	CB	GLU	A	245	26.908	32.177	50.421	1.00 30.22
ATOM	1909	CG	GLU	A	245	25.701	32.938	49.842	1.00 39.79
ATOM	1910	CD	GLU	A	245	26.026	33.564	48.529	1.00 51.91
ATOM	1911	OE1	GLU	A	245	26.945	34.351	48.358	1.00 34.19
ATOM	1912	OE2	GLU	A	245	25.246	33.142	47.585	1.00 47.48
ATOM	1913	N	ASP	A	246	28.570	30.484	52.680	1.00 32.29
ATOM	1914	CA	ASP	A	246	29.417	29.350	53.033	1.00 30.70
ATOM	1915	C	ASP	A	246	28.848	28.645	54.230	1.00 35.47
ATOM	1916	O	ASP	A	246	28.881	27.417	54.347	1.00 37.08
ATOM	1917	CB	ASP	A	246	30.873	29.717	53.355	1.00 33.17
ATOM	1918	CG	ASP	A	246	31.709	28.473	53.413	1.00 64.49
ATOM	1919	OD1	ASP	A	246	31.934	27.789	52.437	1.00 67.15
ATOM	1920	OD2	ASP	A	246	32.118	28.167	54.622	1.00 79.01
ATOM	1921	N	LEU	A	247	28.323	29.434	55.134	1.00 33.59
ATOM	1922	CA	LEU	A	247	27.731	28.868	56.334	1.00 36.70
ATOM	1923	C	LEU	A	247	26.355	28.208	56.083	1.00 35.92
ATOM	1924	O	LEU	A	247	26.060	27.110	56.551	1.00 30.77
ATOM	1925	CB	LEU	A	247	27.562	29.954	57.435	1.00 38.34
ATOM	1926	CG	LEU	A	247	28.732	30.100	58.394	1.00 44.30
ATOM	1927	CD1	LEU	A	247	29.341	28.738	58.641	1.00 48.20
ATOM	1928	CD2	LEU	A	247	29.779	31.013	57.815	1.00 35.25
ATOM	1929	N	GLY	A	248	25.471	28.887	55.353	1.00 34.97
ATOM	1930	CA	GLY	A	248	24.160	28.315	55.181	1.00 36.00
ATOM	1931	C	GLY	A	248	23.754	27.976	53.778	1.00 37.99
ATOM	1932	O	GLY	A	248	22.637	27.524	53.526	1.00 38.13
ATOM	1933	N	GLY	A	249	24.637	28.158	52.849	1.00 30.74
ATOM	1934	CA	GLY	A	249	24.203	27.852	51.526	1.00 30.15
ATOM	1935	C	GLY	A	249	23.918	29.131	50.759	1.00 38.91
ATOM	1936	O	GLY	A	249	24.126	30.240	51.238	1.00 41.32
ATOM	1937	N	PRO	A	250	23.453	28.946	49.547	1.00 38.93
ATOM	1938	CA	PRO	A	250	23.173	30.021	48.639	1.00 38.03
ATOM	1939	C	PRO	A	250	22.203	31.078	49.096	1.00 42.17
ATOM	1940	O	PRO	A	250	21.258	30.823	49.840	1.00 45.20
ATOM	1941	CB	PRO	A	250	22.663	29.357	47.352	1.00 39.18
ATOM	1942	CG	PRO	A	250	22.952	27.864	47.436	1.00 41.01
ATOM	1943	CD	PRO	A	250	23.396	27.610	48.865	1.00 38.57
ATOM	1944	N	TYR	A	251	22.486	32.275	48.600	1.00 35.37
ATOM	1945	CA	TYR	A	251	21.692	33.461	48.817	1.00 34.87
ATOM	1946	C	TYR	A	251	20.740	33.479	47.649	1.00 39.55
ATOM	1947	O	TYR	A	251	21.125	33.794	46.535	1.00 42.57
ATOM	1948	CB	TYR	A	251	22.540	34.759	48.790	1.00 35.07
ATOM	1949	CG	TYR	A	251	21.711	35.980	49.119	1.00 35.25
ATOM	1950	CD1	TYR	A	251	21.341	36.229	50.441	1.00 33.14
ATOM	1951	CD2	TYR	A	251	21.260	36.846	48.121	1.00 37.98
ATOM	1952	CE1	TYR	A	251	20.575	37.341	50.781	1.00 28.05
ATOM	1953	CE2	TYR	A	251	20.492	37.967	48.443	1.00 40.05

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ATOM   1954  CZ  TYR A 251      20.160  38.213  49.777  1.00 42.84
ATOM   1955  OH  TYR A 251      19.409  39.307  50.112  1.00 39.70
ATOM   1956  N   VAL A 252      19.510  33.102  47.914  1.00 32.21
ATOM   1957  CA  VAL A 252      18.495  33.003  46.899  1.00 30.05
ATOM   1958  C   VAL A 252      17.708  34.279  46.631  1.00 38.47
ATOM   1959  O   VAL A 252      17.000  34.340  45.640  1.00 40.65
ATOM   1960  CB  VAL A 252      17.560  31.845  47.253  1.00 31.27
ATOM   1961  CG1 VAL A 252      18.378  30.605  47.643  1.00 28.15
ATOM   1962  CG2 VAL A 252      16.614  32.234  48.405  1.00 30.93
ATOM   1963  N   TRP A 253      17.800  35.292  47.504  1.00 32.44
ATOM   1964  CA  TRP A 253      17.041  36.509  47.309  1.00 30.93
ATOM   1965  C   TRP A 253      17.468  37.341  46.119  1.00 43.56
ATOM   1966  O   TRP A 253      16.690  38.119  45.568  1.00 46.70
ATOM   1967  CB  TRP A 253      16.898  37.302  48.606  1.00 29.65
ATOM   1968  CG  TRP A 253      16.364  36.369  49.625  1.00 30.19
ATOM   1969  CD1 TRP A 253      17.086  35.546  50.413  1.00 32.81
ATOM   1970  CD2 TRP A 253      14.989  36.110  49.913  1.00 29.63
ATOM   1971  NE1 TRP A 253      16.251  34.794  51.194  1.00 30.69
ATOM   1972  CE2 TRP A 253      14.955  35.128  50.912  1.00 31.50
ATOM   1973  CE3 TRP A 253      13.789  36.637  49.450  1.00 30.18
ATOM   1974  CZ2 TRP A 253      13.746  34.657  51.433  1.00 30.31
ATOM   1975  CZ3 TRP A 253      12.600  36.164  49.958  1.00 31.14
ATOM   1976  CH2 TRP A 253      12.579  35.176  50.946  1.00 31.37
ATOM   1977  N   GLY A 254      18.697  37.182  45.675  1.00 42.35
ATOM   1978  CA  GLY A 254      19.101  37.944  44.509  1.00 41.34
ATOM   1979  C   GLY A 254      19.875  39.192  44.858  1.00 45.47
ATOM   1980  O   GLY A 254      21.079  39.236  44.671  1.00 45.89
ATOM   1981  N   GLN A 255      19.160  40.210  45.351  1.00 41.86
ATOM   1982  CA  GLN A 255      19.746  41.488  45.675  1.00 38.67
ATOM   1983  C   GLN A 255      19.576  41.776  47.153  1.00 40.18
ATOM   1984  O   GLN A 255      18.494  41.811  47.659  1.00 38.67
ATOM   1985  CB  GLN A 255      19.023  42.552  44.836  1.00 37.82
ATOM   1986  CG  GLN A 255      19.455  43.979  45.169  1.00 50.17
ATOM   1987  CD  GLN A 255      20.618  44.368  44.283  1.00 62.88
ATOM   1988  OE1 GLN A 255      21.104  43.612  43.463  1.00 55.76
ATOM   1989  NE2 GLN A 255      21.057  45.625  44.479  1.00 34.97
ATOM   1990  N   TYR A 256      20.716  41.900  47.866  1.00 33.01
ATOM   1991  CA  TYR A 256      20.651  42.361  49.258  1.00 28.69
ATOM   1992  C   TYR A 256      20.891  43.854  49.329  1.00 26.72
ATOM   1993  O   TYR A 256      21.963  44.321  49.225  1.00 24.22
ATOM   1994  CB  TYR A 256      21.743  41.629  50.075  1.00 29.99
ATOM   1995  CG  TYR A 256      21.567  41.867  51.556  1.00 35.47
ATOM   1996  CD1 TYR A 256      20.582  41.200  52.250  1.00 35.76
ATOM   1997  CD2 TYR A 256      22.405  42.746  52.239  1.00 37.52
ATOM   1998  CE1 TYR A 256      20.436  41.396  53.599  1.00 25.80
ATOM   1999  CE2 TYR A 256      22.255  42.946  53.588  1.00 39.10
ATOM   2000  CZ  TYR A 256      21.283  42.275  54.268  1.00 31.78
ATOM   2001  OH  TYR A 256      21.153  42.433  55.631  1.00 37.35
ATOM   2002  N   ASP A 257      19.834  44.613  49.463  1.00 23.26
ATOM   2003  CA  ASP A 257      20.077  46.027  49.621  1.00 23.47
ATOM   2004  C   ASP A 257      19.977  46.444  51.071  1.00 35.90
ATOM   2005  O   ASP A 257      19.729  45.661  51.967  1.00 39.48
ATOM   2006  CB  ASP A 257      19.073  46.803  48.758  1.00 24.13
ATOM   2007  CG  ASP A 257      19.689  47.030  47.388  1.00 38.50
ATOM   2008  OD1 ASP A 257      20.843  46.675  47.220  1.00 42.61
ATOM   2009  OD2 ASP A 257      19.020  47.555  46.517  1.00 29.02
ATOM   2010  N   LEU A 258      20.370  47.661  51.386  1.00 30.86
ATOM   2011  CA  LEU A 258      20.306  48.159  52.735  1.00 27.50
ATOM   2012  C   LEU A 258      19.526  49.466  52.765  1.00 36.37
ATOM   2013  O   LEU A 258      19.620  50.302  51.840  1.00 37.98
ATOM   2014  CB  LEU A 258      21.727  48.442  53.274  1.00 24.71
ATOM   2015  CG  LEU A 258      22.552  47.191  53.491  1.00 31.13
ATOM   2016  CD1 LEU A 258      23.913  47.567  54.043  1.00 30.89
ATOM   2017  CD2 LEU A 258      21.854  46.282  54.500  1.00 33.65
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ATOM	2018	N	LEU	A	259	18.762	49.632	53.838	1.00 29.87
ATOM	2019	CA	LEU	A	259	18.006	50.849	54.052	1.00 28.43
ATOM	2020	C	LEU	A	259	18.283	51.453	55.446	1.00 31.30
ATOM	2021	O	LEU	A	259	18.055	50.819	56.477	1.00 31.19
ATOM	2022	CB	LEU	A	259	16.500	50.809	53.693	1.00 27.63
ATOM	2023	CG	LEU	A	259	15.706	51.980	54.298	1.00 31.51
ATOM	2024	CD1	LEU	A	259	16.026	53.300	53.605	1.00 32.32
ATOM	2025	CD2	LEU	A	259	14.212	51.731	54.253	1.00 26.87
ATOM	2026	N	VAL	A	260	18.807	52.683	55.447	1.00 25.88
ATOM	2027	CA	VAL	A	260	19.105	53.435	56.638	1.00 25.99
ATOM	2028	C	VAL	A	260	17.896	54.336	56.796	1.00 34.83
ATOM	2029	O	VAL	A	260	17.647	55.187	55.959	1.00 41.92
ATOM	2030	CB	VAL	A	260	20.390	54.234	56.408	1.00 29.97
ATOM	2031	CG1	VAL	A	260	20.701	55.179	57.592	1.00 32.08
ATOM	2032	CG2	VAL	A	260	21.563	53.295	56.130	1.00 26.15
ATOM	2033	N	LEU	A	261	17.098	54.120	57.815	1.00 28.41
ATOM	2034	CA	LEU	A	261	15.865	54.878	58.024	1.00 25.52
ATOM	2035	C	LEU	A	261	16.016	56.054	58.948	1.00 29.42
ATOM	2036	O	LEU	A	261	17.090	56.300	59.489	1.00 29.96
ATOM	2037	CB	LEU	A	261	14.874	53.921	58.706	1.00 25.70
ATOM	2038	CG	LEU	A	261	14.387	52.877	57.740	1.00 33.14
ATOM	2039	CD1	LEU	A	261	15.161	51.571	57.929	1.00 32.73
ATOM	2040	CD2	LEU	A	261	12.900	52.686	57.935	1.00 43.74
ATOM	2041	N	PRO	A	262	14.903	56.758	59.142	1.00 28.52
ATOM	2042	CA	PRO	A	262	14.894	57.870	60.047	1.00 28.50
ATOM	2043	C	PRO	A	262	15.152	57.294	61.432	1.00 35.36
ATOM	2044	O	PRO	A	262	14.866	56.124	61.683	1.00 34.52
ATOM	2045	CB	PRO	A	262	13.512	58.512	59.971	1.00 29.19
ATOM	2046	CG	PRO	A	262	12.707	57.719	58.964	1.00 34.34
ATOM	2047	CD	PRO	A	262	13.581	56.575	58.492	1.00 30.63
ATOM	2048	N	PRO	A	263	15.706	58.105	62.327	1.00 31.50
ATOM	2049	CA	PRO	A	263	16.060	57.657	63.673	1.00 28.77
ATOM	2050	C	PRO	A	263	14.966	57.021	64.493	1.00 29.15
ATOM	2051	O	PRO	A	263	15.256	56.335	65.434	1.00 26.36
ATOM	2052	CB	PRO	A	263	16.652	58.867	64.392	1.00 29.16
ATOM	2053	CG	PRO	A	263	16.851	59.954	63.335	1.00 31.55
ATOM	2054	CD	PRO	A	263	15.994	59.558	62.138	1.00 29.17
ATOM	2055	N	SER	A	264	13.712	57.258	64.143	1.00 33.87
ATOM	2056	CA	SER	A	264	12.578	56.703	64.864	1.00 33.81
ATOM	2057	C	SER	A	264	12.403	55.223	64.604	1.00 37.36
ATOM	2058	O	SER	A	264	11.529	54.570	65.201	1.00 39.61
ATOM	2059	CB	SER	A	264	11.280	57.423	64.576	1.00 35.61
ATOM	2060	OG	SER	A	264	10.955	57.276	63.201	1.00 53.45
ATOM	2061	N	PHE	A	265	13.213	54.684	63.710	1.00 29.00
ATOM	2062	CA	PHE	A	265	13.136	53.256	63.453	1.00 28.56
ATOM	2063	C	PHE	A	265	13.260	52.491	64.787	1.00 28.49
ATOM	2064	O	PHE	A	265	14.208	52.675	65.533	1.00 27.36
ATOM	2065	CB	PHE	A	265	14.200	52.833	62.454	1.00 31.40
ATOM	2066	CG	PHE	A	265	13.875	51.458	62.028	1.00 34.51
ATOM	2067	CD1	PHE	A	265	12.601	51.174	61.543	1.00 35.11
ATOM	2068	CD2	PHE	A	265	14.814	50.435	62.156	1.00 38.94
ATOM	2069	CE1	PHE	A	265	12.282	49.876	61.154	1.00 37.42
ATOM	2070	CE2	PHE	A	265	14.511	49.131	61.772	1.00 42.65
ATOM	2071	CZ	PHE	A	265	13.236	48.860	61.274	1.00 40.14
ATOM	2072	N	PRO	A	266	12.272	51.650	65.128	1.00 24.06
ATOM	2073	CA	PRO	A	266	12.249	50.945	66.419	1.00 20.62
ATOM	2074	C	PRO	A	266	13.231	49.794	66.701	1.00 29.34
ATOM	2075	O	PRO	A	266	13.343	49.364	67.847	1.00 28.17
ATOM	2076	CB	PRO	A	266	10.808	50.463	66.593	1.00 19.16
ATOM	2077	CG	PRO	A	266	10.076	50.686	65.281	1.00 21.07
ATOM	2078	CD	PRO	A	266	11.046	51.355	64.325	1.00 19.44
ATOM	2079	N	TYR	A	267	13.922	49.280	65.676	1.00 27.23
ATOM	2080	CA	TYR	A	267	14.849	48.160	65.817	1.00 25.74
ATOM	2081	C	TYR	A	267	16.181	48.454	65.189	1.00 32.57

ATOM	2082	O	TYR	A	267	16.281	49.316	64.324	1.00 32.48
ATOM	2083	CB	TYR	A	267	14.298	46.903	65.121	1.00 25.07
ATOM	2084	CG	TYR	A	267	12.968	46.502	65.674	1.00 24.45
ATOM	2085	CD1	TYR	A	267	12.915	45.765	66.856	1.00 27.05
ATOM	2086	CD2	TYR	A	267	11.776	46.851	65.037	1.00 22.15
ATOM	2087	CE1	TYR	A	267	11.697	45.387	67.419	1.00 25.01
ATOM	2088	CE2	TYR	A	267	10.548	46.496	65.596	1.00 19.09
ATOM	2089	CZ	TYR	A	267	10.510	45.767	66.786	1.00 17.98
ATOM	2090	OH	TYR	A	267	9.302	45.416	67.353	1.00 19.51
ATOM	2091	N	GLY	A	268	17.196	47.698	65.627	1.00 30.22
ATOM	2092	CA	GLY	A	268	18.547	47.826	65.114	1.00 27.29
ATOM	2093	C	GLY	A	268	18.485	47.620	63.614	1.00 29.82
ATOM	2094	O	GLY	A	268	19.136	48.297	62.836	1.00 32.99
ATOM	2095	N	GLY	A	269	17.637	46.676	63.228	1.00 23.19
ATOM	2096	CA	GLY	A	269	17.393	46.320	61.853	1.00 21.62
ATOM	2097	C	GLY	A	269	16.187	45.402	61.777	1.00 27.53
ATOM	2098	O	GLY	A	269	15.681	44.948	62.820	1.00 20.14
ATOM	2099	N	MET	A	270	15.735	45.154	60.528	1.00 27.81
ATOM	2100	CA	MET	A	270	14.615	44.267	60.176	1.00 25.61
ATOM	2101	C	MET	A	270	14.956	43.585	58.874	1.00 33.56
ATOM	2102	O	MET	A	270	15.221	44.247	57.867	1.00 34.67
ATOM	2103	CB	MET	A	270	13.247	44.936	60.028	1.00 26.07
ATOM	2104	CG	MET	A	270	12.195	43.937	59.602	1.00 28.81
ATOM	2105	SD	MET	A	270	11.875	42.742	60.929	1.00 37.39
ATOM	2106	CE	MET	A	270	10.720	41.621	60.082	1.00 35.30
ATOM	2107	N	GLU	A	271	14.995	42.263	58.904	1.00 32.20
ATOM	2108	CA	GLU	A	271	15.393	41.459	57.753	1.00 33.32
ATOM	2109	C	GLU	A	271	14.419	41.382	56.567	1.00 40.86
ATOM	2110	O	GLU	A	271	14.087	40.285	56.107	1.00 42.02
ATOM	2111	CB	GLU	A	271	15.802	40.054	58.230	1.00 35.05
ATOM	2112	CG	GLU	A	271	14.607	39.218	58.760	1.00 33.55
ATOM	2113	CD	GLU	A	271	14.291	39.428	60.219	1.00 25.52
ATOM	2114	OE1	GLU	A	271	14.586	40.436	60.844	1.00 37.23
ATOM	2115	OE2	GLU	A	271	13.699	38.393	60.757	1.00 25.86
ATOM	2116	N	ASN	A	272	13.978	42.535	56.052	1.00 35.34
ATOM	2117	CA	ASN	A	272	13.057	42.544	54.928	1.00 33.26
ATOM	2118	C	ASN	A	272	13.787	42.048	53.702	1.00 34.47
ATOM	2119	O	ASN	A	272	14.811	42.613	53.351	1.00 33.64
ATOM	2120	CB	ASN	A	272	12.441	43.947	54.719	1.00 30.65
ATOM	2121	CG	ASN	A	272	11.667	44.453	55.935	1.00 42.50
ATOM	2122	OD1	ASN	A	272	11.908	45.554	56.475	1.00 47.09
ATOM	2123	ND2	ASN	A	272	10.716	43.661	56.371	1.00 24.31
ATOM	2124	N	PRO	A	273	13.281	40.983	53.078	1.00 29.63
ATOM	2125	CA	PRO	A	273	13.935	40.373	51.910	1.00 28.47
ATOM	2126	C	PRO	A	273	14.303	41.345	50.819	1.00 30.43
ATOM	2127	O	PRO	A	273	13.457	42.089	50.372	1.00 31.65
ATOM	2128	CB	PRO	A	273	12.991	39.305	51.381	1.00 30.16
ATOM	2129	CG	PRO	A	273	11.829	39.237	52.365	1.00 36.65
ATOM	2130	CD	PRO	A	273	11.927	40.440	53.310	1.00 30.84
ATOM	2131	N	CYS	A	274	15.571	41.333	50.431	1.00 27.40
ATOM	2132	CA	CYS	A	274	16.069	42.206	49.373	1.00 28.17
ATOM	2133	C	CYS	A	274	16.327	43.604	49.860	1.00 27.35
ATOM	2134	O	CYS	A	274	17.114	44.345	49.248	1.00 28.53
ATOM	2135	CB	CYS	A	274	15.121	42.347	48.145	1.00 32.00
ATOM	2136	SG	CYS	A	274	14.659	40.798	47.340	1.00 38.42
ATOM	2137	N	LEU	A	275	15.658	43.972	50.947	1.00 26.20
ATOM	2138	CA	LEU	A	275	15.789	45.315	51.535	1.00 29.54
ATOM	2139	C	LEU	A	275	15.857	45.279	53.059	1.00 32.52
ATOM	2140	O	LEU	A	275	14.859	45.250	53.772	1.00 32.44
ATOM	2141	CB	LEU	A	275	14.657	46.253	51.005	1.00 28.58
ATOM	2142	CG	LEU	A	275	14.847	47.735	51.239	1.00 26.78
ATOM	2143	CD1	LEU	A	275	16.191	48.183	50.698	1.00 21.90
ATOM	2144	CD2	LEU	A	275	13.712	48.478	50.554	1.00 31.48
ATOM	2145	N	THR	A	276	17.062	45.244	53.570	1.00 29.67

ATOM	2146	CA	THR	A	276	17.225	45.198	54.996	1.00 30.47
ATOM	2147	C	THR	A	276	17.120	46.624	55.597	1.00 34.60
ATOM	2148	O	THR	A	276	17.766	47.588	55.129	1.00 31.01
ATOM	2149	CB	THR	A	276	18.508	44.397	55.387	1.00 30.98
ATOM	2150	OG1	THR	A	276	18.224	43.030	55.512	1.00 42.01
ATOM	2151	CG2	THR	A	276	19.124	44.835	56.694	1.00 29.43
ATOM	2152	N	PHE	A	277	16.280	46.759	56.622	1.00 27.69
ATOM	2153	CA	PHE	A	277	16.164	48.034	57.274	1.00 28.92
ATOM	2154	C	PHE	A	277	17.184	48.065	58.403	1.00 36.07
ATOM	2155	O	PHE	A	277	17.337	47.088	59.131	1.00 34.57
ATOM	2156	CB	PHE	A	277	14.791	48.265	57.901	1.00 30.17
ATOM	2157	CG	PHE	A	277	13.774	48.458	56.848	1.00 30.72
ATOM	2158	CD1	PHE	A	277	14.011	47.966	55.568	1.00 30.73
ATOM	2159	CD2	PHE	A	277	12.573	49.114	57.105	1.00 30.61
ATOM	2160	CE1	PHE	A	277	13.072	48.135	54.552	1.00 29.30
ATOM	2161	CE2	PHE	A	277	11.619	49.276	56.101	1.00 32.26
ATOM	2162	CZ	PHE	A	277	11.862	48.772	54.824	1.00 27.48
ATOM	2163	N	VAL	A	278	17.864	49.186	58.562	1.00 32.97
ATOM	2164	CA	VAL	A	278	18.839	49.338	59.614	1.00 32.66
ATOM	2165	C	VAL	A	278	18.696	50.698	60.248	1.00 37.01
ATOM	2166	O	VAL	A	278	18.251	51.635	59.599	1.00 37.16
ATOM	2167	CB	VAL	A	278	20.246	49.088	59.109	1.00 36.51
ATOM	2168	CG1	VAL	A	278	20.173	47.967	58.086	1.00 37.40
ATOM	2169	CG2	VAL	A	278	20.791	50.356	58.444	1.00 34.87
ATOM	2170	N	THR	A	279	19.066	50.778	61.515	1.00 32.36
ATOM	2171	CA	THR	A	279	18.948	51.994	62.264	1.00 31.03
ATOM	2172	C	THR	A	279	20.121	52.883	62.035	1.00 37.42
ATOM	2173	O	THR	A	279	21.243	52.397	61.920	1.00 39.87
ATOM	2174	CB	THR	A	279	18.885	51.695	63.759	1.00 31.39
ATOM	2175	OG1	THR	A	279	19.110	52.895	64.472	1.00 34.21
ATOM	2176	CG2	THR	A	279	19.989	50.706	64.083	1.00 23.69
ATOM	2177	N	PRO	A	280	19.845	54.187	62.000	1.00 30.07
ATOM	2178	CA	PRO	A	280	20.903	55.132	61.802	1.00 27.00
ATOM	2179	C	PRO	A	280	21.823	55.110	63.005	1.00 30.60
ATOM	2180	O	PRO	A	280	22.951	55.588	62.934	1.00 30.20
ATOM	2181	CB	PRO	A	280	20.249	56.497	61.601	1.00 26.23
ATOM	2182	CG	PRO	A	280	18.769	56.337	61.889	1.00 28.07
ATOM	2183	CD	PRO	A	280	18.499	54.848	61.984	1.00 26.11
ATOM	2184	N	THR	A	281	21.348	54.509	64.112	1.00 27.82
ATOM	2185	CA	THR	A	281	22.199	54.426	65.302	1.00 27.48
ATOM	2186	C	THR	A	281	23.372	53.523	65.073	1.00 31.37
ATOM	2187	O	THR	A	281	24.226	53.385	65.944	1.00 31.93
ATOM	2188	CB	THR	A	281	21.499	54.016	66.601	1.00 21.45
ATOM	2189	OG1	THR	A	281	21.021	52.681	66.524	1.00 33.18
ATOM	2190	CG2	THR	A	281	20.388	54.994	66.874	1.00 9.89
ATOM	2191	N	LEU	A	282	23.378	52.881	63.913	1.00 25.29
ATOM	2192	CA	LEU	A	282	24.473	51.993	63.586	1.00 24.04
ATOM	2193	C	LEU	A	282	25.682	52.790	63.049	1.00 34.74
ATOM	2194	O	LEU	A	282	26.787	52.279	62.884	1.00 34.84
ATOM	2195	CB	LEU	A	282	24.063	51.038	62.464	1.00 22.14
ATOM	2196	CG	LEU	A	282	23.104	49.916	62.819	1.00 26.88
ATOM	2197	CD1	LEU	A	282	23.312	48.809	61.791	1.00 27.77
ATOM	2198	CD2	LEU	A	282	23.322	49.404	64.249	1.00 21.75
ATOM	2199	N	LEU	A	283	25.465	54.063	62.744	1.00 32.05
ATOM	2200	CA	LEU	A	283	26.501	54.903	62.159	1.00 31.43
ATOM	2201	C	LEU	A	283	27.659	55.324	63.055	1.00 41.94
ATOM	2202	O	LEU	A	283	27.907	56.525	63.196	1.00 49.19
ATOM	2203	CB	LEU	A	283	25.861	56.117	61.418	1.00 29.55
ATOM	2204	CG	LEU	A	283	24.720	55.661	60.488	1.00 32.94
ATOM	2205	CD1	LEU	A	283	23.933	56.811	59.869	1.00 33.48
ATOM	2206	CD2	LEU	A	283	25.232	54.716	59.409	1.00 28.39
ATOM	2207	N	ALA	A	284	28.387	54.370	63.638	1.00 33.18
ATOM	2208	CA	ALA	A	284	29.488	54.728	64.532	1.00 30.20
ATOM	2209	C	ALA	A	284	30.655	55.492	63.922	1.00 31.97

ATOM	2210	O	ALA	A	284	31.411	56.165	64.642	1.00 31.40
ATOM	2211	CB	ALA	A	284	29.973	53.544	65.336	1.00 29.60
ATOM	2212	N	GLY	A	285	30.801	55.371	62.605	1.00 27.10
ATOM	2213	CA	GLY	A	285	31.882	56.018	61.867	1.00 29.77
ATOM	2214	C	GLY	A	285	33.174	55.194	61.910	1.00 39.25
ATOM	2215	O	GLY	A	285	34.264	55.649	61.544	1.00 41.21
ATOM	2216	N	ASP	A	286	33.022	53.951	62.363	1.00 34.57
ATOM	2217	CA	ASP	A	286	34.144	53.057	62.473	1.00 32.57
ATOM	2218	C	ASP	A	286	33.805	51.625	62.130	1.00 31.59
ATOM	2219	O	ASP	A	286	34.609	50.743	62.325	1.00 29.27
ATOM	2220	CB	ASP	A	286	34.812	53.163	63.860	1.00 34.65
ATOM	2221	CG	ASP	A	286	34.081	52.447	64.945	1.00 41.93
ATOM	2222	OD1	ASP	A	286	33.008	51.893	64.765	1.00 45.21
ATOM	2223	OD2	ASP	A	286	34.714	52.492	66.087	1.00 35.67
ATOM	2224	N	LYS	A	287	32.590	51.395	61.641	1.00 29.46
ATOM	2225	CA	LYS	A	287	32.199	50.038	61.272	1.00 31.62
ATOM	2226	C	LYS	A	287	31.976	49.060	62.437	1.00 37.91
ATOM	2227	O	LYS	A	287	31.761	47.879	62.240	1.00 37.91
ATOM	2228	CB	LYS	A	287	33.215	49.447	60.304	1.00 32.17
ATOM	2229	CG	LYS	A	287	33.510	50.358	59.119	1.00 51.60
ATOM	2230	CD	LYS	A	287	33.960	49.601	57.877	1.00 50.74
ATOM	2231	CE	LYS	A	287	35.290	50.105	57.328	1.00 63.80
ATOM	2232	NZ	LYS	A	287	35.167	50.866	56.069	1.00 71.91
ATOM	2233	N	SER	A	288	32.168	49.575	63.647	1.00 31.58
ATOM	2234	CA	SER	A	288	32.079	48.737	64.810	1.00 27.15
ATOM	2235	C	SER	A	288	30.742	48.137	65.142	1.00 36.08
ATOM	2236	O	SER	A	288	30.676	47.318	66.057	1.00 37.87
ATOM	2237	CB	SER	A	288	32.618	49.463	66.005	1.00 16.31
ATOM	2238	OG	SER	A	288	31.659	50.443	66.312	1.00 29.71
ATOM	2239	N	LEU	A	289	29.669	48.529	64.460	1.00 29.34
ATOM	2240	CA	LEU	A	289	28.351	47.979	64.794	1.00 24.70
ATOM	2241	C	LEU	A	289	27.792	47.105	63.686	1.00 32.97
ATOM	2242	O	LEU	A	289	26.591	46.766	63.648	1.00 30.35
ATOM	2243	CB	LEU	A	289	27.385	49.090	65.191	1.00 21.45
ATOM	2244	CG	LEU	A	289	27.954	49.887	66.347	1.00 22.99
ATOM	2245	CD1	LEU	A	289	26.881	50.769	66.950	1.00 20.66
ATOM	2246	CD2	LEU	A	289	28.381	48.881	67.394	1.00 29.65
ATOM	2247	N	SER	A	290	28.723	46.753	62.801	1.00 31.21
ATOM	2248	CA	SER	A	290	28.453	45.941	61.645	1.00 29.89
ATOM	2249	C	SER	A	290	27.861	44.582	62.006	1.00 30.57
ATOM	2250	O	SER	A	290	27.299	43.872	61.153	1.00 29.73
ATOM	2251	CB	SER	A	290	29.704	45.800	60.783	1.00 29.27
ATOM	2252	OG	SER	A	290	30.470	44.725	61.266	1.00 38.77
ATOM	2253	N	ASN	A	291	27.980	44.207	63.282	1.00 26.55
ATOM	2254	CA	ASN	A	291	27.449	42.909	63.706	1.00 25.78
ATOM	2255	C	ASN	A	291	26.006	42.773	63.355	1.00 30.89
ATOM	2256	O	ASN	A	291	25.576	41.702	62.975	1.00 29.73
ATOM	2257	CB	ASN	A	291	27.725	42.503	65.157	1.00 28.48
ATOM	2258	CG	ASN	A	291	26.910	43.313	66.119	1.00 33.33
ATOM	2259	OD1	ASN	A	291	27.065	44.529	66.198	1.00 34.48
ATOM	2260	ND2	ASN	A	291	26.001	42.653	66.818	1.00 28.96
ATOM	2261	N	VAL	A	292	25.277	43.885	63.476	1.00 30.68
ATOM	2262	CA	VAL	A	292	23.865	43.924	63.142	1.00 30.27
ATOM	2263	C	VAL	A	292	23.667	43.619	61.669	1.00 32.61
ATOM	2264	O	VAL	A	292	22.644	43.082	61.255	1.00 33.31
ATOM	2265	CB	VAL	A	292	23.288	45.289	63.505	1.00 35.13
ATOM	2266	CG1	VAL	A	292	21.877	45.486	62.946	1.00 33.48
ATOM	2267	CG2	VAL	A	292	23.328	45.478	65.014	1.00 35.02
ATOM	2268	N	ILE	A	293	24.653	43.975	60.861	1.00 27.92
ATOM	2269	CA	ILE	A	293	24.527	43.685	59.461	1.00 28.71
ATOM	2270	C	ILE	A	293	24.658	42.159	59.296	1.00 35.03
ATOM	2271	O	ILE	A	293	23.860	41.475	58.624	1.00 38.34
ATOM	2272	CB	ILE	A	293	25.554	44.438	58.606	1.00 33.84
ATOM	2273	CG1	ILE	A	293	25.608	45.952	58.898	1.00 34.55

ATOM	2274	CG2	ILE	A	293	25.305	44.186	57.121	1.00 36.50
ATOM	2275	CD1	ILE	A	293	24.265	46.680	58.808	1.00 30.49
ATOM	2276	N	ALA	A	294	25.668	41.584	59.934	1.00 23.76
ATOM	2277	CA	ALA	A	294	25.836	40.138	59.809	1.00 19.95
ATOM	2278	C	ALA	A	294	24.559	39.409	60.165	1.00 27.33
ATOM	2279	O	ALA	A	294	24.183	38.422	59.505	1.00 25.48
ATOM	2280	CB	ALA	A	294	26.984	39.644	60.688	1.00 19.24
ATOM	2281	N	HIS	A	295	23.917	39.934	61.244	1.00 27.63
ATOM	2282	CA	HIS	A	295	22.666	39.414	61.797	1.00 26.83
ATOM	2283	C	HIS	A	295	21.611	39.383	60.734	1.00 28.61
ATOM	2284	O	HIS	A	295	21.169	38.301	60.348	1.00 25.72
ATOM	2285	CB	HIS	A	295	22.148	40.175	63.028	1.00 27.98
ATOM	2286	CG	HIS	A	295	20.937	39.534	63.657	1.00 31.62
ATOM	2287	ND1	HIS	A	295	21.047	38.675	64.763	1.00 32.66
ATOM	2288	CD2	HIS	A	295	19.602	39.643	63.338	1.00 30.92
ATOM	2289	CE1	HIS	A	295	19.802	38.298	65.088	1.00 30.14
ATOM	2290	NE2	HIS	A	295	18.916	38.860	64.254	1.00 30.24
ATOM	2291	N	GLU	A	296	21.257	40.590	60.251	1.00 27.23
ATOM	2292	CA	GLU	A	296	20.266	40.749	59.195	1.00 25.98
ATOM	2293	C	GLU	A	296	20.533	39.790	58.056	1.00 32.73
ATOM	2294	O	GLU	A	296	19.628	39.081	57.561	1.00 31.88
ATOM	2295	CB	GLU	A	296	20.046	42.203	58.728	1.00 24.55
ATOM	2296	CG	GLU	A	296	19.892	43.148	59.936	1.00 23.16
ATOM	2297	CD	GLU	A	296	18.939	42.632	60.991	1.00 53.50
ATOM	2298	OE1	GLU	A	296	17.964	41.956	60.700	1.00 23.99
ATOM	2299	OE2	GLU	A	296	19.237	43.006	62.233	1.00 32.77
ATOM	2300	N	ILE	A	297	21.803	39.745	57.675	1.00 25.37
ATOM	2301	CA	ILE	A	297	22.195	38.870	56.599	1.00 22.64
ATOM	2302	C	ILE	A	297	21.812	37.445	56.859	1.00 27.47
ATOM	2303	O	ILE	A	297	21.175	36.799	56.048	1.00 26.25
ATOM	2304	CB	ILE	A	297	23.672	38.963	56.302	1.00 24.19
ATOM	2305	CG1	ILE	A	297	23.920	40.140	55.355	1.00 25.28
ATOM	2306	CG2	ILE	A	297	24.079	37.686	55.626	1.00 20.77
ATOM	2307	CD1	ILE	A	297	25.325	40.705	55.435	1.00 16.26
ATOM	2308	N	SER	A	298	22.226	36.947	58.012	1.00 28.23
ATOM	2309	CA	SER	A	298	21.939	35.569	58.377	1.00 25.04
ATOM	2310	C	SER	A	298	20.467	35.235	58.298	1.00 26.21
ATOM	2311	O	SER	A	298	20.118	34.097	58.000	1.00 26.30
ATOM	2312	CB	SER	A	298	22.520	35.209	59.714	1.00 27.82
ATOM	2313	OG	SER	A	298	23.890	35.552	59.714	1.00 35.98
ATOM	2314	N	HIS	A	299	19.599	36.230	58.562	1.00 22.17
ATOM	2315	CA	HIS	A	299	18.205	36.092	58.719	1.00 22.77
ATOM	2316	C	HIS	A	299	17.614	35.710	57.387	1.00 29.10
ATOM	2317	O	HIS	A	299	16.553	35.162	57.290	1.00 31.50
ATOM	2318	CB	HIS	A	299	17.662	37.432	59.200	1.00 24.67
ATOM	2319	CG	HIS	A	299	17.053	37.338	60.602	1.00 29.10
ATOM	2320	ND1	HIS	A	299	16.190	36.368	60.975	1.00 30.70
ATOM	2321	CD2	HIS	A	299	17.196	38.233	61.667	1.00 32.39
ATOM	2322	CE1	HIS	A	299	15.811	36.675	62.233	1.00 30.41
ATOM	2323	NE2	HIS	A	299	16.397	37.783	62.674	1.00 31.74
ATOM	2324	N	SER	A	300	18.356	36.048	56.315	1.00 23.31
ATOM	2325	CA	SER	A	300	17.942	35.581	55.010	1.00 24.24
ATOM	2326	C	SER	A	300	17.879	34.050	54.977	1.00 34.13
ATOM	2327	O	SER	A	300	17.075	33.463	54.305	1.00 33.28
ATOM	2328	CB	SER	A	300	18.941	36.092	53.965	1.00 27.31
ATOM	2329	OG	SER	A	300	18.947	37.519	53.962	1.00 49.96
ATOM	2330	N	TRP	A	301	18.773	33.411	55.752	1.00 33.09
ATOM	2331	CA	TRP	A	301	18.702	31.969	55.829	1.00 31.84
ATOM	2332	C	TRP	A	301	17.740	31.511	56.895	1.00 32.15
ATOM	2333	O	TRP	A	301	16.764	30.876	56.620	1.00 27.05
ATOM	2334	CB	TRP	A	301	20.095	31.429	56.082	1.00 30.16
ATOM	2335	CG	TRP	A	301	20.791	31.421	54.801	1.00 32.02
ATOM	2336	CD1	TRP	A	301	20.787	30.393	53.859	1.00 35.05
ATOM	2337	CD2	TRP	A	301	21.496	32.520	54.202	1.00 30.84

ATOM	2338	NE1	TRP	A	301	21.415	30.732	52.722	1.00	33.29
ATOM	2339	CE2	TRP	A	301	21.886	32.112	52.921	1.00	33.44
ATOM	2340	CE3	TRP	A	301	21.811	33.790	54.631	1.00	32.65
ATOM	2341	CZ2	TRP	A	301	22.577	32.970	52.108	1.00	32.21
ATOM	2342	CZ3	TRP	A	301	22.503	34.652	53.812	1.00	36.10
ATOM	2343	CH2	TRP	A	301	22.888	34.239	52.544	1.00	36.83
ATOM	2344	N	THR	A	302	18.042	31.864	58.146	1.00	31.77
ATOM	2345	CA	THR	A	302	17.125	31.488	59.215	1.00	33.55
ATOM	2346	C	THR	A	302	16.276	32.690	59.695	1.00	36.35
ATOM	2347	O	THR	A	302	16.759	33.590	60.330	1.00	36.56
ATOM	2348	CB	THR	A	302	17.963	30.920	60.366	1.00	31.04
ATOM	2349	OG1	THR	A	302	19.047	31.807	60.639	1.00	38.50
ATOM	2350	CG2	THR	A	302	18.544	29.555	59.967	1.00	17.10
ATOM	2351	N	GLY	A	303	15.053	32.418	59.250	1.00	25.28
ATOM	2352	CA	GLY	A	303	13.908	33.236	59.483	1.00	21.59
ATOM	2353	C	GLY	A	303	13.202	33.382	58.163	1.00	26.99
ATOM	2354	O	GLY	A	303	12.040	33.040	57.994	1.00	26.18
ATOM	2355	N	ASN	A	304	13.936	33.891	57.195	1.00	28.05
ATOM	2356	CA	ASN	A	304	13.363	34.101	55.875	1.00	28.17
ATOM	2357	C	ASN	A	304	13.141	32.839	55.056	1.00	28.99
ATOM	2358	O	ASN	A	304	12.118	32.715	54.415	1.00	24.87
ATOM	2359	CB	ASN	A	304	14.091	35.176	55.047	1.00	23.55
ATOM	2360	CG	ASN	A	304	14.133	36.499	55.757	1.00	37.80
ATOM	2361	OD1	ASN	A	304	13.630	36.613	56.892	1.00	20.66
ATOM	2362	ND2	ASN	A	304	14.752	37.488	55.093	1.00	24.17
ATOM	2363	N	LEU	A	305	14.110	31.919	55.055	1.00	27.24
ATOM	2364	CA	LEU	A	305	13.987	30.677	54.306	1.00	27.34
ATOM	2365	C	LEU	A	305	13.218	29.665	55.121	1.00	31.29
ATOM	2366	O	LEU	A	305	12.235	29.051	54.678	1.00	29.23
ATOM	2367	CB	LEU	A	305	15.371	30.119	53.967	1.00	27.62
ATOM	2368	CG	LEU	A	305	15.805	30.593	52.603	1.00	32.23
ATOM	2369	CD1	LEU	A	305	17.289	30.293	52.412	1.00	28.91
ATOM	2370	CD2	LEU	A	305	14.951	29.887	51.549	1.00	41.51
ATOM	2371	N	VAL	A	306	13.711	29.528	56.347	1.00	27.75
ATOM	2372	CA	VAL	A	306	13.134	28.652	57.327	1.00	29.99
ATOM	2373	C	VAL	A	306	12.578	29.527	58.403	1.00	31.78
ATOM	2374	O	VAL	A	306	13.306	30.217	59.110	1.00	28.32
ATOM	2375	CB	VAL	A	306	14.092	27.593	57.827	1.00	37.24
ATOM	2376	CG1	VAL	A	306	15.479	28.180	57.969	1.00	38.36
ATOM	2377	CG2	VAL	A	306	13.602	27.107	59.164	1.00	37.56
ATOM	2378	N	THR	A	307	11.259	29.517	58.440	1.00	29.40
ATOM	2379	CA	THR	A	307	10.499	30.358	59.320	1.00	28.14
ATOM	2380	C	THR	A	307	9.729	29.712	60.446	1.00	34.06
ATOM	2381	O	THR	A	307	9.029	28.706	60.277	1.00	36.72
ATOM	2382	CB	THR	A	307	9.474	31.115	58.460	1.00	23.03
ATOM	2383	OG1	THR	A	307	10.124	31.811	57.422	1.00	28.56
ATOM	2384	CG2	THR	A	307	8.665	32.068	59.336	1.00	12.55
ATOM	2385	N	ASN	A	308	9.802	30.347	61.608	1.00	29.29
ATOM	2386	CA	ASN	A	308	9.042	29.862	62.724	1.00	27.82
ATOM	2387	C	ASN	A	308	7.576	29.716	62.234	1.00	31.42
ATOM	2388	O	ASN	A	308	7.072	30.535	61.450	1.00	32.96
ATOM	2389	CB	ASN	A	308	9.194	30.790	63.972	1.00	23.57
ATOM	2390	CG	ASN	A	308	8.935	32.298	63.745	1.00	30.38
ATOM	2391	OD1	ASN	A	308	9.505	33.190	64.400	1.00	23.70
ATOM	2392	ND2	ASN	A	308	8.056	32.608	62.818	1.00	41.34
ATOM	2393	N	LYS	A	309	6.890	28.658	62.640	1.00	24.10
ATOM	2394	CA	LYS	A	309	5.502	28.433	62.230	1.00	23.40
ATOM	2395	C	LYS	A	309	4.514	29.380	62.964	1.00	28.17
ATOM	2396	O	LYS	A	309	3.430	29.756	62.474	1.00	22.88
ATOM	2397	CB	LYS	A	309	5.151	26.975	62.459	1.00	24.26
ATOM	2398	CG	LYS	A	309	4.036	26.478	61.555	1.00	28.57
ATOM	2399	CD	LYS	A	309	3.543	25.075	61.924	1.00	38.25
ATOM	2400	CE	LYS	A	309	3.475	24.112	60.739	1.00	78.39
ATOM	2401	NZ	LYS	A	309	4.389	22.953	60.849	1.00	98.22

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ATOM   2402  N   THR A 310       4.917  29.744  64.179  1.00 23.46
ATOM   2403  CA  THR A 310       4.179  30.616  65.037  1.00 22.98
ATOM   2404  C   THR A 310       5.142  31.336  65.922  1.00 31.43
ATOM   2405  O   THR A 310       6.223  30.836  66.230  1.00 31.51
ATOM   2406  CB  THR A 310       3.104  29.917  65.871  1.00 34.01
ATOM   2407  OG1 THR A 310       3.684  29.148  66.945  1.00 27.97
ATOM   2408  CG2 THR A 310       2.174  29.114  64.956  1.00 24.58
ATOM   2409  N   TRP A 311       4.733  32.527  66.299  1.00 29.82
ATOM   2410  CA  TRP A 311       5.559  33.371  67.120  1.00 30.49
ATOM   2411  C   TRP A 311       6.044  32.692  68.381  1.00 26.99
ATOM   2412  O   TRP A 311       7.015  33.101  68.971  1.00 25.15
ATOM   2413  CB  TRP A 311       4.933  34.768  67.320  1.00 30.34
ATOM   2414  CG  TRP A 311       4.706  35.412  66.001  1.00 30.63
ATOM   2415  CD1 TRP A 311       3.514  35.785  65.490  1.00 32.07
ATOM   2416  CD2 TRP A 311       5.705  35.723  65.008  1.00 31.31
ATOM   2417  NE1 TRP A 311       3.703  36.335  64.250  1.00 29.97
ATOM   2418  CE2 TRP A 311       5.033  36.317  63.931  1.00 32.88
ATOM   2419  CE3 TRP A 311       7.099  35.586  64.943  1.00 31.44
ATOM   2420  CZ2 TRP A 311       5.721  36.771  62.804  1.00 31.56
ATOM   2421  CZ3 TRP A 311       7.779  36.059  63.848  1.00 30.39
ATOM   2422  CH2 TRP A 311       7.089  36.639  62.789  1.00 30.58
ATOM   2423  N   ASP A 312       5.366  31.632  68.770  1.00 27.36
ATOM   2424  CA  ASP A 312       5.757  30.868  69.950  1.00 27.38
ATOM   2425  C   ASP A 312       7.149  30.213  69.757  1.00 31.25
ATOM   2426  O   ASP A 312       7.826  29.802  70.718  1.00 27.07
ATOM   2427  CB  ASP A 312       4.697  29.750  70.217  1.00 25.96
ATOM   2428  CG  ASP A 312       3.432  30.230  70.872  1.00 27.42
ATOM   2429  OD1 ASP A 312       3.197  31.396  71.102  1.00 28.97
ATOM   2430  OD2 ASP A 312       2.623  29.265  71.208  1.00 29.33
ATOM   2431  N   HIS A 313       7.562  30.089  68.487  1.00 25.04
ATOM   2432  CA  HIS A 313       8.820  29.454  68.164  1.00 23.48
ATOM   2433  C   HIS A 313       9.864  30.452  67.737  1.00 25.38
ATOM   2434  O   HIS A 313      10.929  30.139  67.214  1.00 29.97
ATOM   2435  CB  HIS A 313       8.588  28.245  67.209  1.00 25.00
ATOM   2436  CG  HIS A 313       7.641  27.230  67.837  1.00 29.77
ATOM   2437  ND1 HIS A 313       8.087  26.183  68.635  1.00 31.37
ATOM   2438  CD2 HIS A 313       6.279  27.152  67.808  1.00 31.31
ATOM   2439  CE1 HIS A 313       7.015  25.509  69.039  1.00 28.91
ATOM   2440  NE2 HIS A 313       5.913  26.066  68.559  1.00 29.40
ATOM   2441  N   PHE A 314       9.521  31.682  68.005  1.00 17.43
ATOM   2442  CA  PHE A 314      10.345  32.810  67.701  1.00 17.16
ATOM   2443  C   PHE A 314      11.852  32.523  67.812  1.00 26.01
ATOM   2444  O   PHE A 314      12.669  32.922  66.963  1.00 30.40
ATOM   2445  CB  PHE A 314       9.908  34.056  68.517  1.00 18.63
ATOM   2446  CG  PHE A 314      10.592  35.351  68.113  1.00 20.10
ATOM   2447  CD1 PHE A 314      10.712  35.697  66.768  1.00 21.80
ATOM   2448  CD2 PHE A 314      11.129  36.214  69.070  1.00 22.60
ATOM   2449  CE1 PHE A 314      11.337  36.890  66.400  1.00 24.74
ATOM   2450  CE2 PHE A 314      11.750  37.416  68.716  1.00 27.24
ATOM   2451  CZ  PHE A 314      11.857  37.756  67.368  1.00 24.97
ATOM   2452  N   TRP A 315      12.235  31.828  68.861  1.00 19.66
ATOM   2453  CA  TRP A 315      13.639  31.541  69.068  1.00 17.87
ATOM   2454  C   TRP A 315      14.292  30.775  67.953  1.00 28.55
ATOM   2455  O   TRP A 315      15.518  30.769  67.830  1.00 29.23
ATOM   2456  CB  TRP A 315      13.860  30.842  70.362  1.00 16.03
ATOM   2457  CG  TRP A 315      13.613  29.408  70.161  1.00 19.64
ATOM   2458  CD1 TRP A 315      12.428  28.787  70.247  1.00 22.39
ATOM   2459  CD2 TRP A 315      14.599  28.430  69.876  1.00 21.70
ATOM   2460  NE1 TRP A 315      12.597  27.457  70.033  1.00 24.22
ATOM   2461  CE2 TRP A 315      13.934  27.205  69.801  1.00 27.96
ATOM   2462  CE3 TRP A 315      15.976  28.481  69.681  1.00 22.89
ATOM   2463  CZ2 TRP A 315      14.631  26.018  69.547  1.00 27.76
ATOM   2464  CZ3 TRP A 315      16.651  27.321  69.421  1.00 23.16
ATOM   2465  CH2 TRP A 315      15.991  26.108  69.341  1.00 23.94
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ATOM	2466	N	LEU	A	316	13.488	30.114	67.144	1.00 26.33
ATOM	2467	CA	LEU	A	316	14.092	29.400	66.067	1.00 25.44
ATOM	2468	C	LEU	A	316	14.666	30.443	65.129	1.00 33.21
ATOM	2469	O	LEU	A	316	15.737	30.252	64.530	1.00 37.80
ATOM	2470	CB	LEU	A	316	13.050	28.567	65.311	1.00 24.82
ATOM	2471	CG	LEU	A	316	12.663	27.242	65.956	1.00 27.62
ATOM	2472	CD1	LEU	A	316	11.574	26.552	65.106	1.00 22.30
ATOM	2473	CD2	LEU	A	316	13.897	26.344	66.097	1.00 27.03
ATOM	2474	N	ASN	A	317	13.931	31.555	64.997	1.00 20.55
ATOM	2475	CA	ASN	A	317	14.354	32.624	64.115	1.00 19.34
ATOM	2476	C	ASN	A	317	15.603	33.333	64.531	1.00 30.38
ATOM	2477	O	ASN	A	317	16.553	33.425	63.766	1.00 32.04
ATOM	2478	CB	ASN	A	317	13.273	33.682	63.838	1.00 14.82
ATOM	2479	CG	ASN	A	317	12.330	33.177	62.793	1.00 31.14
ATOM	2480	OD1	ASN	A	317	12.151	31.966	62.657	1.00 38.42
ATOM	2481	ND2	ASN	A	317	11.724	34.074	62.049	1.00 17.34
ATOM	2482	N	GLU	A	318	15.562	33.870	65.750	1.00 26.15
ATOM	2483	CA	GLU	A	318	16.624	34.648	66.358	1.00 20.23
ATOM	2484	C	GLU	A	318	17.860	33.884	66.816	1.00 23.53
ATOM	2485	O	GLU	A	318	19.006	34.273	66.554	1.00 26.34
ATOM	2486	CB	GLU	A	318	15.998	35.484	67.456	1.00 19.11
ATOM	2487	CG	GLU	A	318	14.999	36.480	66.800	1.00 24.06
ATOM	2488	CD	GLU	A	318	15.615	37.391	65.758	1.00 40.32
ATOM	2489	OE1	GLU	A	318	16.833	37.559	65.612	1.00 21.24
ATOM	2490	OE2	GLU	A	318	14.703	38.025	65.062	1.00 24.23
ATOM	2491	N	GLY	A	319	17.621	32.782	67.494	1.00 17.17
ATOM	2492	CA	GLY	A	319	18.681	31.955	68.016	1.00 15.31
ATOM	2493	C	GLY	A	319	19.673	31.601	66.953	1.00 24.07
ATOM	2494	O	GLY	A	319	20.860	31.897	67.080	1.00 28.47
ATOM	2495	N	HIS	A	320	19.165	30.956	65.907	1.00 20.24
ATOM	2496	CA	HIS	A	320	19.977	30.556	64.790	1.00 20.13
ATOM	2497	C	HIS	A	320	20.678	31.759	64.142	1.00 24.97
ATOM	2498	O	HIS	A	320	21.855	31.700	63.739	1.00 23.54
ATOM	2499	CB	HIS	A	320	19.143	29.737	63.791	1.00 20.57
ATOM	2500	CG	HIS	A	320	18.662	28.426	64.349	1.00 22.57
ATOM	2501	ND1	HIS	A	320	17.471	28.332	65.058	1.00 22.98
ATOM	2502	CD2	HIS	A	320	19.217	27.176	64.286	1.00 19.52
ATOM	2503	CE1	HIS	A	320	17.336	27.046	65.385	1.00 19.18
ATOM	2504	NE2	HIS	A	320	18.368	26.329	64.952	1.00 18.12
ATOM	2505	N	THR	A	321	19.958	32.875	64.053	1.00 21.61
ATOM	2506	CA	THR	A	321	20.543	34.056	63.478	1.00 22.16
ATOM	2507	C	THR	A	321	21.697	34.552	64.342	1.00 27.47
ATOM	2508	O	THR	A	321	22.789	34.825	63.836	1.00 26.64
ATOM	2509	CB	THR	A	321	19.470	35.097	63.113	1.00 27.88
ATOM	2510	OG1	THR	A	321	18.403	34.392	62.523	1.00 27.92
ATOM	2511	CG2	THR	A	321	19.999	36.088	62.087	1.00 18.05
ATOM	2512	N	VAL	A	322	21.496	34.634	65.659	1.00 21.90
ATOM	2513	CA	VAL	A	322	22.610	35.054	66.470	1.00 19.44
ATOM	2514	C	VAL	A	322	23.762	34.071	66.285	1.00 24.43
ATOM	2515	O	VAL	A	322	24.926	34.414	66.188	1.00 21.48
ATOM	2516	CB	VAL	A	322	22.218	35.185	67.928	1.00 20.92
ATOM	2517	CG1	VAL	A	322	23.406	35.644	68.772	1.00 18.37
ATOM	2518	CG2	VAL	A	322	21.093	36.200	68.048	1.00 20.01
ATOM	2519	N	TYR	A	323	23.427	32.811	66.197	1.00 27.08
ATOM	2520	CA	TYR	A	323	24.446	31.803	66.013	1.00 26.26
ATOM	2521	C	TYR	A	323	25.222	32.036	64.728	1.00 28.26
ATOM	2522	O	TYR	A	323	26.431	31.894	64.643	1.00 27.51
ATOM	2523	CB	TYR	A	323	23.804	30.407	66.020	1.00 25.74
ATOM	2524	CG	TYR	A	323	24.867	29.341	65.987	1.00 26.66
ATOM	2525	CD1	TYR	A	323	25.539	28.957	67.150	1.00 29.09
ATOM	2526	CD2	TYR	A	323	25.199	28.713	64.789	1.00 24.52
ATOM	2527	CE1	TYR	A	323	26.530	27.974	67.157	1.00 22.56
ATOM	2528	CE2	TYR	A	323	26.178	27.722	64.770	1.00 25.31
ATOM	2529	CZ	TYR	A	323	26.846	27.370	65.944	1.00 29.19

ATOM	2530	OH	TYR	A	323	27.823	26.434	65.895	1.00 27.51
ATOM	2531	N	LEU	A	324	24.497	32.408	63.702	1.00 24.82
ATOM	2532	CA	LEU	A	324	25.135	32.638	62.439	1.00 26.04
ATOM	2533	C	LEU	A	324	25.832	33.952	62.417	1.00 30.92
ATOM	2534	O	LEU	A	324	26.903	34.045	61.851	1.00 33.76
ATOM	2535	CB	LEU	A	324	24.176	32.537	61.235	1.00 26.21
ATOM	2536	CG	LEU	A	324	23.916	31.112	60.778	1.00 28.46
ATOM	2537	CD1	LEU	A	324	22.752	31.109	59.791	1.00 28.95
ATOM	2538	CD2	LEU	A	324	25.169	30.508	60.151	1.00 26.54
ATOM	2539	N	GLU	A	325	25.234	34.976	63.033	1.00 27.04
ATOM	2540	CA	GLU	A	325	25.870	36.303	63.064	1.00 22.88
ATOM	2541	C	GLU	A	325	27.282	36.210	63.624	1.00 28.76
ATOM	2542	O	GLU	A	325	28.250	36.722	63.026	1.00 26.24
ATOM	2543	CB	GLU	A	325	25.016	37.365	63.759	1.00 22.01
ATOM	2544	CG	GLU	A	325	25.827	38.411	64.524	1.00 41.55
ATOM	2545	CD	GLU	A	325	25.035	39.040	65.646	1.00 72.11
ATOM	2546	OE1	GLU	A	325	23.866	38.764	65.862	1.00 41.88
ATOM	2547	OE2	GLU	A	325	25.719	39.922	66.350	1.00 67.15
ATOM	2548	N	ARG	A	326	27.349	35.479	64.755	1.00 27.84
ATOM	2549	CA	ARG	A	326	28.551	35.213	65.511	1.00 28.10
ATOM	2550	C	ARG	A	326	29.604	34.457	64.771	1.00 30.90
ATOM	2551	O	ARG	A	326	30.763	34.747	64.976	1.00 33.93
ATOM	2552	CB	ARG	A	326	28.334	34.761	66.947	1.00 31.52
ATOM	2553	CG	ARG	A	326	27.645	35.864	67.726	1.00 22.20
ATOM	2554	CD	ARG	A	326	27.462	35.572	69.203	1.00 28.71
ATOM	2555	NE	ARG	A	326	26.727	36.673	69.830	1.00 23.82
ATOM	2556	CZ	ARG	A	326	25.805	36.556	70.780	1.00 26.09
ATOM	2557	NH1	ARG	A	326	25.443	35.388	71.305	1.00 23.16
ATOM	2558	NH2	ARG	A	326	25.220	37.655	71.222	1.00 24.77
ATOM	2559	N	HIS	A	327	29.221	33.511	63.918	1.00 29.85
ATOM	2560	CA	HIS	A	327	30.207	32.777	63.120	1.00 30.52
ATOM	2561	C	HIS	A	327	30.778	33.738	62.085	1.00 35.50
ATOM	2562	O	HIS	A	327	31.966	33.777	61.822	1.00 36.74
ATOM	2563	CB	HIS	A	327	29.591	31.555	62.407	1.00 31.59
ATOM	2564	CG	HIS	A	327	29.764	30.259	63.176	1.00 34.51
ATOM	2565	ND1	HIS	A	327	30.963	29.913	63.788	1.00 36.17
ATOM	2566	CD2	HIS	A	327	28.875	29.263	63.432	1.00 35.58
ATOM	2567	CE1	HIS	A	327	30.778	28.740	64.384	1.00 35.27
ATOM	2568	NE2	HIS	A	327	29.532	28.322	64.191	1.00 35.56
ATOM	2569	N	ILE	A	328	29.902	34.549	61.511	1.00 31.10
ATOM	2570	CA	ILE	A	328	30.328	35.517	60.528	1.00 31.66
ATOM	2571	C	ILE	A	328	31.416	36.407	61.086	1.00 40.12
ATOM	2572	O	ILE	A	328	32.451	36.615	60.465	1.00 40.81
ATOM	2573	CB	ILE	A	328	29.175	36.379	59.998	1.00 32.94
ATOM	2574	CG1	ILE	A	328	28.220	35.570	59.114	1.00 29.53
ATOM	2575	CG2	ILE	A	328	29.694	37.591	59.201	1.00 30.91
ATOM	2576	CD1	ILE	A	328	27.119	36.463	58.535	1.00 32.98
ATOM	2577	N	CYS	A	329	31.179	36.948	62.266	1.00 37.88
ATOM	2578	CA	CYS	A	329	32.170	37.810	62.851	1.00 39.54
ATOM	2579	C	CYS	A	329	33.475	37.092	63.157	1.00 40.19
ATOM	2580	O	CYS	A	329	34.567	37.642	62.971	1.00 38.44
ATOM	2581	CB	CYS	A	329	31.607	38.509	64.083	1.00 42.61
ATOM	2582	SG	CYS	A	329	30.241	39.595	63.619	1.00 48.14
ATOM	2583	N	GLY	A	330	33.332	35.852	63.632	1.00 34.74
ATOM	2584	CA	GLY	A	330	34.471	35.030	63.980	1.00 35.20
ATOM	2585	C	GLY	A	330	35.359	34.854	62.778	1.00 43.66
ATOM	2586	O	GLY	A	330	36.581	34.857	62.891	1.00 46.79
ATOM	2587	N	ARG	A	331	34.709	34.725	61.622	1.00 34.99
ATOM	2588	CA	ARG	A	331	35.416	34.562	60.392	1.00 33.19
ATOM	2589	C	ARG	A	331	36.086	35.863	60.017	1.00 40.63
ATOM	2590	O	ARG	A	331	37.238	35.914	59.586	1.00 44.40
ATOM	2591	CB	ARG	A	331	34.494	34.101	59.269	1.00 31.29
ATOM	2592	CG	ARG	A	331	33.987	32.685	59.450	1.00 47.66
ATOM	2593	CD	ARG	A	331	34.812	31.722	58.622	1.00 70.36

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ATOM   2594  NE  ARG A 331      34.461  31.851  57.221  1.00 80.25
ATOM   2595  CZ  ARG A 331      33.615  31.023  56.628  1.00100.00
ATOM   2596  NH1 ARG A 331      33.055  29.999  57.279  1.00 79.12
ATOM   2597  NH2 ARG A 331      33.334  31.216  55.341  1.00 89.33
ATOM   2598  N   LEU A 332      35.342  36.926  60.172  1.00 32.14
ATOM   2599  CA  LEU A 332      35.885  38.198  59.820  1.00 30.02
ATOM   2600  C   LEU A 332      37.013  38.612  60.761  1.00 40.33
ATOM   2601  O   LEU A 332      38.084  38.972  60.286  1.00 40.10
ATOM   2602  CB  LEU A 332      34.772  39.262  59.822  1.00 28.20
ATOM   2603  CG  LEU A 332      34.451  39.896  58.469  1.00 28.82
ATOM   2604  CD1 LEU A 332      35.007  39.063  57.341  1.00 23.73
ATOM   2605  CD2 LEU A 332      32.947  40.114  58.306  1.00 29.76
ATOM   2606  N   PHE A 333      36.744  38.557  62.091  1.00 37.69
ATOM   2607  CA  PHE A 333      37.657  38.997  63.143  1.00 34.12
ATOM   2608  C   PHE A 333      38.251  37.956  64.035  1.00 37.99
ATOM   2609  O   PHE A 333      39.015  38.293  64.925  1.00 41.67
ATOM   2610  CB  PHE A 333      36.970  40.058  64.024  1.00 35.62
ATOM   2611  CG  PHE A 333      36.209  41.003  63.138  1.00 39.09
ATOM   2612  CD1 PHE A 333      36.887  41.923  62.332  1.00 43.22
ATOM   2613  CD2 PHE A 333      34.818  40.941  63.045  1.00 42.78
ATOM   2614  CE1 PHE A 333      36.205  42.781  61.464  1.00 44.14
ATOM   2615  CE2 PHE A 333      34.123  41.806  62.194  1.00 46.56
ATOM   2616  CZ  PHE A 333      34.814  42.716  61.389  1.00 43.20
ATOM   2617  N   GLY A 334      37.908  36.706  63.865  1.00 34.36
ATOM   2618  CA  GLY A 334      38.507  35.705  64.763  1.00 32.89
ATOM   2619  C   GLY A 334      37.582  34.985  65.767  1.00 32.67
ATOM   2620  O   GLY A 334      36.641  35.540  66.340  1.00 33.48
ATOM   2621  N   GLU A 335      37.908  33.726  66.003  1.00 23.52
ATOM   2622  CA  GLU A 335      37.196  32.875  66.931  1.00 18.13
ATOM   2623  C   GLU A 335      37.278  33.384  68.346  1.00 29.15
ATOM   2624  O   GLU A 335      36.357  33.124  69.112  1.00 34.14
ATOM   2625  CB  GLU A 335      37.782  31.488  66.929  1.00 17.35
ATOM   2626  CG  GLU A 335      37.041  30.591  67.929  1.00 32.97
ATOM   2627  CD  GLU A 335      35.642  30.305  67.473  1.00 46.14
ATOM   2628  OE1 GLU A 335      35.093  30.944  66.588  1.00 39.31
ATOM   2629  OE2 GLU A 335      35.080  29.317  68.132  1.00 32.80
ATOM   2630  N   LYS A 336      38.370  34.077  68.706  1.00 24.53
ATOM   2631  CA  LYS A 336      38.468  34.609  70.061  1.00 25.38
ATOM   2632  C   LYS A 336      37.445  35.726  70.169  1.00 35.32
ATOM   2633  O   LYS A 336      36.908  36.004  71.233  1.00 38.14
ATOM   2634  CB  LYS A 336      39.820  35.199  70.421  1.00 25.45
ATOM   2635  CG  LYS A 336      40.871  34.188  70.825  1.00 25.43
ATOM   2636  CD  LYS A 336      42.207  34.846  71.189  1.00 47.10
ATOM   2637  CE  LYS A 336      43.325  34.600  70.172  1.00 68.74
ATOM   2638  NZ  LYS A 336      44.566  34.072  70.767  1.00 77.62
ATOM   2639  N   PHE A 337      37.174  36.364  69.029  1.00 31.52
ATOM   2640  CA  PHE A 337      36.186  37.442  68.967  1.00 29.34
ATOM   2641  C   PHE A 337      34.783  36.869  69.083  1.00 31.73
ATOM   2642  O   PHE A 337      33.908  37.424  69.742  1.00 35.53
ATOM   2643  CB  PHE A 337      36.304  38.336  67.709  1.00 30.04
ATOM   2644  CG  PHE A 337      35.435  39.589  67.747  1.00 35.16
ATOM   2645  CD1 PHE A 337      35.468  40.459  68.843  1.00 43.88
ATOM   2646  CD2 PHE A 337      34.550  39.893  66.709  1.00 40.16
ATOM   2647  CE1 PHE A 337      34.688  41.617  68.913  1.00 46.53
ATOM   2648  CE2 PHE A 337      33.753  41.040  66.760  1.00 45.62
ATOM   2649  CZ  PHE A 337      33.830  41.908  67.852  1.00 45.57
ATOM   2650  N   ARG A 338      34.566  35.733  68.452  1.00 25.52
ATOM   2651  CA  ARG A 338      33.266  35.119  68.508  1.00 25.23
ATOM   2652  C   ARG A 338      32.944  34.759  69.922  1.00 29.77
ATOM   2653  O   ARG A 338      31.854  35.025  70.415  1.00 31.81
ATOM   2654  CB  ARG A 338      33.186  33.920  67.606  1.00 24.04
ATOM   2655  CG  ARG A 338      31.839  33.228  67.623  1.00 21.31
ATOM   2656  CD  ARG A 338      31.807  32.086  66.599  1.00 30.62
ATOM   2657  NE  ARG A 338      32.518  30.892  67.040  1.00 29.87
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ATOM	2658	CZ	ARG	A	338	31.919	29.781	67.466	1.00 26.37
ATOM	2659	NH1	ARG	A	338	30.616	29.687	67.518	1.00 20.26
ATOM	2660	NH2	ARG	A	338	32.632	28.737	67.864	1.00 18.57
ATOM	2661	N	HIS	A	339	33.934	34.190	70.577	1.00 25.88
ATOM	2662	CA	HIS	A	339	33.813	33.797	71.982	1.00 25.59
ATOM	2663	C	HIS	A	339	33.455	34.972	72.892	1.00 27.61
ATOM	2664	O	HIS	A	339	32.615	34.912	73.793	1.00 25.27
ATOM	2665	CB	HIS	A	339	35.065	33.045	72.462	1.00 25.06
ATOM	2666	CG	HIS	A	339	34.923	31.587	72.155	1.00 28.13
ATOM	2667	ND1	HIS	A	339	35.049	30.612	73.127	1.00 30.52
ATOM	2668	CD2	HIS	A	339	34.586	30.970	70.981	1.00 30.89
ATOM	2669	CE1	HIS	A	339	34.843	29.442	72.535	1.00 30.89
ATOM	2670	NE2	HIS	A	339	34.546	29.616	71.245	1.00 31.36
ATOM	2671	N	PHE	A	340	34.103	36.065	72.608	1.00 24.54
ATOM	2672	CA	PHE	A	340	33.892	37.278	73.334	1.00 25.36
ATOM	2673	C	PHE	A	340	32.452	37.762	73.216	1.00 32.47
ATOM	2674	O	PHE	A	340	31.822	38.222	74.190	1.00 32.78
ATOM	2675	CB	PHE	A	340	34.876	38.309	72.801	1.00 26.03
ATOM	2676	CG	PHE	A	340	34.654	39.671	73.346	1.00 26.47
ATOM	2677	CD1	PHE	A	340	35.238	40.047	74.559	1.00 24.59
ATOM	2678	CD2	PHE	A	340	33.902	40.592	72.616	1.00 28.22
ATOM	2679	CE1	PHE	A	340	35.063	41.330	75.072	1.00 21.58
ATOM	2680	CE2	PHE	A	340	33.715	41.879	73.115	1.00 29.13
ATOM	2681	CZ	PHE	A	340	34.280	42.225	74.345	1.00 25.28
ATOM	2682	N	ASN	A	341	31.944	37.663	72.004	1.00 28.41
ATOM	2683	CA	ASN	A	341	30.600	38.084	71.728	1.00 29.60
ATOM	2684	C	ASN	A	341	29.665	37.110	72.379	1.00 38.52
ATOM	2685	O	ASN	A	341	28.699	37.511	73.029	1.00 42.88
ATOM	2686	CB	ASN	A	341	30.322	38.274	70.224	1.00 30.01
ATOM	2687	CG	ASN	A	341	31.159	39.374	69.587	1.00 52.80
ATOM	2688	OD1	ASN	A	341	31.528	39.284	68.404	1.00 60.88
ATOM	2689	ND2	ASN	A	341	31.442	40.427	70.359	1.00 41.02
ATOM	2690	N	ALA	A	342	29.994	35.826	72.239	1.00 28.24
ATOM	2691	CA	ALA	A	342	29.195	34.800	72.877	1.00 26.95
ATOM	2692	C	ALA	A	342	29.013	35.134	74.393	1.00 35.98
ATOM	2693	O	ALA	A	342	27.877	35.261	74.897	1.00 35.09
ATOM	2694	CB	ALA	A	342	29.837	33.422	72.671	1.00 25.45
ATOM	2695	N	LEU	A	343	30.153	35.304	75.122	1.00 29.16
ATOM	2696	CA	LEU	A	343	30.162	35.633	76.560	1.00 22.58
ATOM	2697	C	LEU	A	343	29.310	36.854	76.831	1.00 27.48
ATOM	2698	O	LEU	A	343	28.452	36.821	77.696	1.00 32.73
ATOM	2699	CB	LEU	A	343	31.583	35.786	77.147	1.00 18.70
ATOM	2700	CG	LEU	A	343	31.647	35.693	78.671	1.00 20.08
ATOM	2701	CD1	LEU	A	343	30.842	34.510	79.204	1.00 17.76
ATOM	2702	CD2	LEU	A	343	33.091	35.522	79.111	1.00 21.94
ATOM	2703	N	GLY	A	344	29.512	37.936	76.080	1.00 22.60
ATOM	2704	CA	GLY	A	344	28.670	39.146	76.278	1.00 24.15
ATOM	2705	C	GLY	A	344	27.157	38.824	76.136	1.00 31.38
ATOM	2706	O	GLY	A	344	26.339	39.260	76.943	1.00 32.44
ATOM	2707	N	GLY	A	345	26.806	38.017	75.094	1.00 22.79
ATOM	2708	CA	GLY	A	345	25.451	37.587	74.801	1.00 19.88
ATOM	2709	C	GLY	A	345	24.787	36.994	76.034	1.00 28.37
ATOM	2710	O	GLY	A	345	23.632	37.294	76.325	1.00 27.56
ATOM	2711	N	TRP	A	346	25.547	36.153	76.765	1.00 25.41
ATOM	2712	CA	TRP	A	346	25.082	35.520	77.994	1.00 23.90
ATOM	2713	C	TRP	A	346	24.825	36.541	79.071	1.00 31.54
ATOM	2714	O	TRP	A	346	23.957	36.379	79.924	1.00 29.57
ATOM	2715	CB	TRP	A	346	26.122	34.556	78.562	1.00 21.53
ATOM	2716	CG	TRP	A	346	25.680	33.880	79.837	1.00 21.92
ATOM	2717	CD1	TRP	A	346	25.933	34.335	81.079	1.00 24.36
ATOM	2718	CD2	TRP	A	346	25.004	32.597	80.010	1.00 20.97
ATOM	2719	NE1	TRP	A	346	25.450	33.453	82.008	1.00 23.95
ATOM	2720	CE2	TRP	A	346	24.859	32.388	81.391	1.00 24.13
ATOM	2721	CE3	TRP	A	346	24.488	31.611	79.144	1.00 21.46

ATOM	2722	CZ2	TRP	A	346	24.225	31.244	81.921	1.00 22.89
ATOM	2723	CZ3	TRP	A	346	23.872	30.477	79.662	1.00 22.03
ATOM	2724	CH2	TRP	A	346	23.747	30.286	81.046	1.00 21.87
ATOM	2725	N	GLY	A	347	25.627	37.593	79.039	1.00 29.66
ATOM	2726	CA	GLY	A	347	25.465	38.625	80.042	1.00 29.03
ATOM	2727	C	GLY	A	347	24.156	39.333	79.844	1.00 33.01
ATOM	2728	O	GLY	A	347	23.491	39.647	80.799	1.00 34.17
ATOM	2729	N	GLU	A	348	23.797	39.574	78.581	1.00 30.57
ATOM	2730	CA	GLU	A	348	22.535	40.220	78.250	1.00 29.17
ATOM	2731	C	GLU	A	348	21.423	39.282	78.664	1.00 31.25
ATOM	2732	O	GLU	A	348	20.373	39.663	79.142	1.00 33.71
ATOM	2733	CB	GLU	A	348	22.432	40.606	76.757	1.00 30.33
ATOM	2734	CG	GLU	A	348	23.432	41.715	76.336	1.00 49.41
ATOM	2735	CD	GLU	A	348	23.209	43.088	76.964	1.00 73.39
ATOM	2736	OE1	GLU	A	348	22.295	43.846	76.656	1.00 71.22
ATOM	2737	OE2	GLU	A	348	24.119	43.395	77.857	1.00 44.23
ATOM	2738	N	LEU	A	349	21.682	38.011	78.541	1.00 27.36
ATOM	2739	CA	LEU	A	349	20.677	37.081	78.976	1.00 26.89
ATOM	2740	C	LEU	A	349	20.429	37.250	80.485	1.00 24.87
ATOM	2741	O	LEU	A	349	19.299	37.403	80.914	1.00 28.31
ATOM	2742	CB	LEU	A	349	20.984	35.630	78.529	1.00 27.18
ATOM	2743	CG	LEU	A	349	19.943	34.565	78.942	1.00 32.45
ATOM	2744	CD1	LEU	A	349	18.611	34.704	78.154	1.00 30.09
ATOM	2745	CD2	LEU	A	349	20.541	33.169	78.749	1.00 27.10
ATOM	2746	N	GLN	A	350	21.460	37.255	81.315	1.00 14.78
ATOM	2747	CA	GLN	A	350	21.188	37.428	82.727	1.00 18.51
ATOM	2748	C	GLN	A	350	20.442	38.722	82.953	1.00 25.53
ATOM	2749	O	GLN	A	350	19.495	38.833	83.737	1.00 28.35
ATOM	2750	CB	GLN	A	350	22.469	37.369	83.536	1.00 22.22
ATOM	2751	CG	GLN	A	350	23.512	36.426	82.919	1.00 22.37
ATOM	2752	CD	GLN	A	350	24.871	36.673	83.547	1.00 34.49
ATOM	2753	OE1	GLN	A	350	25.261	35.932	84.417	1.00 24.01
ATOM	2754	NE2	GLN	A	350	25.588	37.727	83.127	1.00 36.58
ATOM	2755	N	ASN	A	351	20.838	39.696	82.201	1.00 22.64
ATOM	2756	CA	ASN	A	351	20.163	40.960	82.273	1.00 26.10
ATOM	2757	C	ASN	A	351	18.661	40.780	82.083	1.00 37.49
ATOM	2758	O	ASN	A	351	17.890	41.098	82.977	1.00 41.41
ATOM	2759	CB	ASN	A	351	20.769	42.021	81.341	1.00 20.74
ATOM	2760	CG	ASN	A	351	22.118	42.477	81.847	1.00 23.25
ATOM	2761	OD1	ASN	A	351	22.692	41.875	82.771	1.00 26.88
ATOM	2762	ND2	ASN	A	351	22.644	43.530	81.247	1.00 32.93
ATOM	2763	N	SER	A	352	18.228	40.252	80.938	1.00 32.84
ATOM	2764	CA	SER	A	352	16.784	40.041	80.715	1.00 34.27
ATOM	2765	C	SER	A	352	16.107	39.135	81.784	1.00 31.72
ATOM	2766	O	SER	A	352	14.927	39.266	82.189	1.00 28.64
ATOM	2767	CB	SER	A	352	16.503	39.531	79.301	1.00 42.57
ATOM	2768	OG	SER	A	352	17.506	39.979	78.407	1.00 49.17
ATOM	2769	N	VAL	A	353	16.874	38.188	82.247	1.00 21.90
ATOM	2770	CA	VAL	A	353	16.322	37.351	83.234	1.00 22.13
ATOM	2771	C	VAL	A	353	16.068	38.122	84.516	1.00 36.22
ATOM	2772	O	VAL	A	353	14.958	38.076	85.052	1.00 37.69
ATOM	2773	CB	VAL	A	353	17.137	36.070	83.419	1.00 20.84
ATOM	2774	CG1	VAL	A	353	16.632	35.256	84.634	1.00 15.06
ATOM	2775	CG2	VAL	A	353	16.968	35.284	82.105	1.00 20.93
ATOM	2776	N	LYS	A	354	17.086	38.847	85.002	1.00 30.67
ATOM	2777	CA	LYS	A	354	16.880	39.587	86.221	1.00 31.71
ATOM	2778	C	LYS	A	354	15.660	40.474	86.098	1.00 36.17
ATOM	2779	O	LYS	A	354	14.808	40.582	86.980	1.00 35.80
ATOM	2780	CB	LYS	A	354	18.099	40.396	86.624	1.00 35.28
ATOM	2781	CG	LYS	A	354	17.841	41.303	87.818	1.00 51.51
ATOM	2782	CD	LYS	A	354	19.038	41.405	88.749	1.00 60.46
ATOM	2783	CE	LYS	A	354	19.198	42.780	89.383	1.00 50.09
ATOM	2784	NZ	LYS	A	354	20.596	43.133	89.657	1.00 63.77
ATOM	2785	N	THR	A	355	15.608	41.108	84.962	1.00 32.63

ATOM	2786	CA	THR	A	355	14.562	42.025	84.610	1.00	34.03
ATOM	2787	C	THR	A	355	13.129	41.422	84.578	1.00	42.11
ATOM	2788	O	THR	A	355	12.216	42.006	85.154	1.00	40.96
ATOM	2789	CB	THR	A	355	14.974	42.736	83.308	1.00	41.11
ATOM	2790	OG1	THR	A	355	16.071	43.615	83.542	1.00	29.85
ATOM	2791	CG2	THR	A	355	13.798	43.438	82.656	1.00	45.50
ATOM	2792	N	PHE	A	356	12.895	40.273	83.908	1.00	33.89
ATOM	2793	CA	PHE	A	356	11.556	39.729	83.860	1.00	29.29
ATOM	2794	C	PHE	A	356	11.209	39.070	85.147	1.00	31.93
ATOM	2795	O	PHE	A	356	10.089	39.152	85.642	1.00	33.85
ATOM	2796	CB	PHE	A	356	11.460	38.645	82.785	1.00	33.30
ATOM	2797	CG	PHE	A	356	11.187	39.196	81.416	1.00	36.54
ATOM	2798	CD1	PHE	A	356	10.106	40.054	81.224	1.00	42.38
ATOM	2799	CD2	PHE	A	356	11.985	38.858	80.320	1.00	38.62
ATOM	2800	CE1	PHE	A	356	9.831	40.596	79.968	1.00	44.75
ATOM	2801	CE2	PHE	A	356	11.723	39.384	79.055	1.00	43.46
ATOM	2802	CZ	PHE	A	356	10.649	40.261	78.890	1.00	43.86
ATOM	2803	N	GLY	A	357	12.212	38.386	85.661	1.00	30.41
ATOM	2804	CA	GLY	A	357	12.152	37.564	86.864	1.00	29.17
ATOM	2805	C	GLY	A	357	12.446	36.100	86.438	1.00	28.92
ATOM	2806	O	GLY	A	357	12.008	35.642	85.372	1.00	27.33
ATOM	2807	N	GLU	A	358	13.211	35.382	87.243	1.00	21.27
ATOM	2808	CA	GLU	A	358	13.590	34.040	86.898	1.00	23.10
ATOM	2809	C	GLU	A	358	12.424	33.104	86.747	1.00	31.53
ATOM	2810	O	GLU	A	358	12.581	31.972	86.294	1.00	30.92
ATOM	2811	CB	GLU	A	358	14.596	33.473	87.880	1.00	25.36
ATOM	2812	CG	GLU	A	358	14.011	33.436	89.301	1.00	38.73
ATOM	2813	CD	GLU	A	358	15.011	33.037	90.345	1.00	56.34
ATOM	2814	OE1	GLU	A	358	16.026	32.446	90.071	1.00	50.55
ATOM	2815	OE2	GLU	A	358	14.678	33.403	91.564	1.00	75.65
ATOM	2816	N	THR	A	359	11.246	33.542	87.139	1.00	27.87
ATOM	2817	CA	THR	A	359	10.154	32.625	86.970	1.00	25.66
ATOM	2818	C	THR	A	359	9.236	33.152	85.906	1.00	25.96
ATOM	2819	O	THR	A	359	8.247	32.528	85.533	1.00	25.58
ATOM	2820	CB	THR	A	359	9.423	32.341	88.253	1.00	25.00
ATOM	2821	OG1	THR	A	359	8.908	33.565	88.692	1.00	33.10
ATOM	2822	CG2	THR	A	359	10.406	31.785	89.273	1.00	14.43
ATOM	2823	N	HIS	A	360	9.602	34.310	85.407	1.00	20.75
ATOM	2824	CA	HIS	A	360	8.837	34.902	84.363	1.00	22.77
ATOM	2825	C	HIS	A	360	8.823	34.034	83.130	1.00	35.30
ATOM	2826	O	HIS	A	360	9.858	33.611	82.620	1.00	37.42
ATOM	2827	CB	HIS	A	360	9.294	36.291	83.982	1.00	23.18
ATOM	2828	CG	HIS	A	360	8.207	36.908	83.219	1.00	27.05
ATOM	2829	ND1	HIS	A	360	7.532	38.009	83.691	1.00	29.34
ATOM	2830	CD2	HIS	A	360	7.651	36.545	82.059	1.00	29.91
ATOM	2831	CE1	HIS	A	360	6.596	38.315	82.806	1.00	27.94
ATOM	2832	NE2	HIS	A	360	6.651	37.440	81.812	1.00	29.60
ATOM	2833	N	PRO	A	361	7.606	33.817	82.666	1.00	32.40
ATOM	2834	CA	PRO	A	361	7.301	32.999	81.519	1.00	29.46
ATOM	2835	C	PRO	A	361	7.862	33.478	80.224	1.00	30.59
ATOM	2836	O	PRO	A	361	7.907	32.737	79.248	1.00	33.00
ATOM	2837	CB	PRO	A	361	5.770	32.963	81.478	1.00	30.74
ATOM	2838	CG	PRO	A	361	5.311	33.172	82.927	1.00	34.96
ATOM	2839	CD	PRO	A	361	6.463	33.869	83.627	1.00	31.82
ATOM	2840	N	PHE	A	362	8.289	34.712	80.179	1.00	26.32
ATOM	2841	CA	PHE	A	362	8.823	35.173	78.933	1.00	25.68
ATOM	2842	C	PHE	A	362	10.261	34.781	78.829	1.00	29.73
ATOM	2843	O	PHE	A	362	10.906	35.131	77.870	1.00	32.02
ATOM	2844	CB	PHE	A	362	8.643	36.677	78.723	1.00	28.12
ATOM	2845	CG	PHE	A	362	7.194	37.105	78.629	1.00	30.03
ATOM	2846	CD1	PHE	A	362	6.204	36.276	78.098	1.00	30.92
ATOM	2847	CD2	PHE	A	362	6.804	38.372	79.051	1.00	32.04
ATOM	2848	CE1	PHE	A	362	4.864	36.655	77.998	1.00	26.59
ATOM	2849	CE2	PHE	A	362	5.470	38.773	78.952	1.00	32.40

ATOM	2914	C	ASP	A	371	-2.557	37.636	75.255	1.00 40.92
ATOM	2915	O	ASP	A	371	-2.784	38.625	75.933	1.00 41.63
ATOM	2916	CB	ASP	A	371	-4.519	36.375	76.245	1.00 39.88
ATOM	2917	CG	ASP	A	371	-5.805	35.733	75.798	1.00 51.30
ATOM	2918	OD1	ASP	A	371	-6.373	36.072	74.761	1.00 50.39
ATOM	2919	OD2	ASP	A	371	-6.206	34.754	76.583	1.00 48.61
ATOM	2920	N	ILE	A	372	-1.387	37.398	74.664	1.00 36.37
ATOM	2921	CA	ILE	A	372	-0.259	38.283	74.817	1.00 34.61
ATOM	2922	C	ILE	A	372	0.203	39.018	73.555	1.00 35.46
ATOM	2923	O	ILE	A	372	0.545	38.400	72.548	1.00 36.69
ATOM	2924	CB	ILE	A	372	0.920	37.511	75.381	1.00 36.51
ATOM	2925	CG1	ILE	A	372	0.658	37.195	76.842	1.00 37.01
ATOM	2926	CG2	ILE	A	372	2.121	38.441	75.281	1.00 35.52
ATOM	2927	CD1	ILE	A	372	1.268	38.261	77.747	1.00 54.33
ATOM	2928	N	ASP	A	373	0.254	40.345	73.601	1.00 25.92
ATOM	2929	CA	ASP	A	373	0.747	41.053	72.450	1.00 23.77
ATOM	2930	C	ASP	A	373	2.263	40.781	72.360	1.00 31.40
ATOM	2931	O	ASP	A	373	3.040	41.002	73.305	1.00 32.80
ATOM	2932	CB	ASP	A	373	0.408	42.543	72.519	1.00 25.08
ATOM	2933	CG	ASP	A	373	1.064	43.356	71.418	1.00 43.24
ATOM	2934	OD1	ASP	A	373	1.861	42.894	70.616	1.00 45.30
ATOM	2935	OD2	ASP	A	373	0.668	44.610	71.395	1.00 38.59
ATOM	2936	N	PRO	A	374	2.709	40.267	71.225	1.00 29.51
ATOM	2937	CA	PRO	A	374	4.123	39.943	71.132	1.00 28.52
ATOM	2938	C	PRO	A	374	5.029	41.090	71.506	1.00 32.54
ATOM	2939	O	PRO	A	374	6.019	40.905	72.217	1.00 29.62
ATOM	2940	CB	PRO	A	374	4.390	39.421	69.714	1.00 28.88
ATOM	2941	CG	PRO	A	374	3.028	39.278	69.032	1.00 32.27
ATOM	2942	CD	PRO	A	374	1.966	39.786	70.008	1.00 28.84
ATOM	2943	N	ASP	A	375	4.660	42.257	70.981	1.00 26.85
ATOM	2944	CA	ASP	A	375	5.357	43.511	71.154	1.00 24.25
ATOM	2945	C	ASP	A	375	5.695	43.783	72.628	1.00 33.10
ATOM	2946	O	ASP	A	375	6.648	44.494	72.988	1.00 30.67
ATOM	2947	CB	ASP	A	375	4.507	44.617	70.509	1.00 24.46
ATOM	2948	CG	ASP	A	375	4.753	44.836	69.033	1.00 30.08
ATOM	2949	OD1	ASP	A	375	5.703	44.393	68.411	1.00 33.47
ATOM	2950	OD2	ASP	A	375	3.852	45.609	68.491	1.00 38.41
ATOM	2951	N	VAL	A	376	4.885	43.161	73.477	1.00 30.21
ATOM	2952	CA	VAL	A	376	5.001	43.232	74.904	1.00 25.40
ATOM	2953	C	VAL	A	376	5.879	42.106	75.431	1.00 37.27
ATOM	2954	O	VAL	A	376	6.599	42.299	76.394	1.00 42.46
ATOM	2955	CB	VAL	A	376	3.638	43.099	75.550	1.00 22.48
ATOM	2956	CG1	VAL	A	376	3.799	42.533	76.975	1.00 21.25
ATOM	2957	CG2	VAL	A	376	2.926	44.440	75.547	1.00 18.29
ATOM	2958	N	ALA	A	377	5.811	40.905	74.831	1.00 30.48
ATOM	2959	CA	ALA	A	377	6.671	39.793	75.288	1.00 27.04
ATOM	2960	C	ALA	A	377	8.149	39.911	74.797	1.00 28.15
ATOM	2961	O	ALA	A	377	9.077	39.325	75.312	1.00 27.36
ATOM	2962	CB	ALA	A	377	6.091	38.433	74.891	1.00 26.74
ATOM	2963	N	TYR	A	378	8.376	40.692	73.768	1.00 25.81
ATOM	2964	CA	TYR	A	378	9.683	40.876	73.161	1.00 25.43
ATOM	2965	C	TYR	A	378	10.862	41.194	74.057	1.00 30.49
ATOM	2966	O	TYR	A	378	10.873	42.204	74.747	1.00 32.35
ATOM	2967	CB	TYR	A	378	9.549	41.924	72.068	1.00 26.20
ATOM	2968	CG	TYR	A	378	10.804	42.168	71.327	1.00 19.90
ATOM	2969	CD1	TYR	A	378	11.256	41.231	70.406	1.00 18.53
ATOM	2970	CD2	TYR	A	378	11.536	43.331	71.543	1.00 18.47
ATOM	2971	CE1	TYR	A	378	12.444	41.436	69.716	1.00 15.98
ATOM	2972	CE2	TYR	A	378	12.719	43.555	70.840	1.00 18.77
ATOM	2973	CZ	TYR	A	378	13.161	42.609	69.920	1.00 16.37
ATOM	2974	OH	TYR	A	378	14.309	42.811	69.212	1.00 32.30
ATOM	2975	N	SER	A	379	11.879	40.317	73.977	1.00 23.03
ATOM	2976	CA	SER	A	379	13.115	40.430	74.725	1.00 18.13
ATOM	2977	C	SER	A	379	14.267	39.777	73.970	1.00 20.60

ATOM	2850	CZ	PHE	A	362	4.495	37.920	78.435	1.00 26.37
ATOM	2851	N	THR	A	363	10.730	34.049	79.843	1.00 27.22
ATOM	2852	CA	THR	A	363	12.102	33.575	79.943	1.00 27.52
ATOM	2853	C	THR	A	363	12.251	32.132	79.504	1.00 29.28
ATOM	2854	O	THR	A	363	13.331	31.560	79.524	1.00 29.42
ATOM	2855	CB	THR	A	363	12.697	33.777	81.360	1.00 31.67
ATOM	2856	OG1	THR	A	363	12.279	32.745	82.218	1.00 26.17
ATOM	2857	CG2	THR	A	363	12.278	35.118	81.930	1.00 31.62
ATOM	2858	N	LYS	A	364	11.148	31.530	79.113	1.00 23.08
ATOM	2859	CA	LYS	A	364	11.174	30.160	78.664	1.00 20.50
ATOM	2860	C	LYS	A	364	11.556	30.270	77.217	1.00 28.83
ATOM	2861	O	LYS	A	364	11.139	31.239	76.570	1.00 29.80
ATOM	2862	CB	LYS	A	364	9.766	29.584	78.667	1.00 23.55
ATOM	2863	CG	LYS	A	364	9.252	29.134	80.022	1.00 40.85
ATOM	2864	CD	LYS	A	364	7.761	29.369	80.162	1.00 44.83
ATOM	2865	CE	LYS	A	364	7.131	28.492	81.224	1.00 66.38
ATOM	2866	NZ	LYS	A	364	6.063	27.638	80.691	1.00 91.70
ATOM	2867	N	LEU	A	365	12.332	29.328	76.698	1.00 23.57
ATOM	2868	CA	LEU	A	365	12.699	29.420	75.312	1.00 23.95
ATOM	2869	C	LEU	A	365	11.414	29.419	74.445	1.00 35.57
ATOM	2870	O	LEU	A	365	11.166	30.369	73.708	1.00 34.58
ATOM	2871	CB	LEU	A	365	13.702	28.303	75.021	1.00 25.08
ATOM	2872	CG	LEU	A	365	14.456	28.372	73.702	1.00 31.15
ATOM	2873	CD1	LEU	A	365	14.987	29.778	73.466	1.00 33.16
ATOM	2874	CD2	LEU	A	365	15.609	27.353	73.781	1.00 30.62
ATOM	2875	N	VAL	A	366	10.572	28.360	74.564	1.00 35.62
ATOM	2876	CA	VAL	A	366	9.294	28.232	73.840	1.00 32.10
ATOM	2877	C	VAL	A	366	8.211	28.911	74.694	1.00 33.14
ATOM	2878	O	VAL	A	366	7.982	28.470	75.808	1.00 34.20
ATOM	2879	CB	VAL	A	366	8.936	26.739	73.568	1.00 34.73
ATOM	2880	CG1	VAL	A	366	7.558	26.605	72.933	1.00 34.88
ATOM	2881	CG2	VAL	A	366	9.922	26.012	72.649	1.00 32.65
ATOM	2882	N	VAL	A	367	7.562	29.990	74.211	1.00 28.76
ATOM	2883	CA	VAL	A	367	6.532	30.700	74.987	1.00 28.27
ATOM	2884	C	VAL	A	367	5.161	30.613	74.420	1.00 30.62
ATOM	2885	O	VAL	A	367	4.994	30.509	73.235	1.00 34.30
ATOM	2886	CB	VAL	A	367	6.773	32.185	75.061	1.00 33.45
ATOM	2887	CG1	VAL	A	367	8.178	32.478	75.565	1.00 33.03
ATOM	2888	CG2	VAL	A	367	6.498	32.804	73.693	1.00 33.18
ATOM	2889	N	ASP	A	368	4.168	30.722	75.290	1.00 29.27
ATOM	2890	CA	ASP	A	368	2.764	30.771	74.984	1.00 27.67
ATOM	2891	C	ASP	A	368	2.315	32.207	74.862	1.00 26.94
ATOM	2892	O	ASP	A	368	2.283	32.975	75.830	1.00 23.11
ATOM	2893	CB	ASP	A	368	1.990	30.073	76.100	1.00 26.80
ATOM	2894	CG	ASP	A	368	0.572	29.781	75.613	1.00 37.90
ATOM	2895	OD1	ASP	A	368	0.276	30.123	74.481	1.00 38.93
ATOM	2896	OD2	ASP	A	368	-0.215	29.217	76.380	1.00 38.59
ATOM	2897	N	LEU	A	369	2.027	32.588	73.622	1.00 26.55
ATOM	2898	CA	LEU	A	369	1.643	33.953	73.373	1.00 27.39
ATOM	2899	C	LEU	A	369	0.138	34.105	73.301	1.00 30.74
ATOM	2900	O	LEU	A	369	-0.372	34.979	72.648	1.00 30.68
ATOM	2901	CB	LEU	A	369	2.281	34.395	72.064	1.00 26.06
ATOM	2902	CG	LEU	A	369	3.759	34.760	72.229	1.00 26.80
ATOM	2903	CD1	LEU	A	369	4.343	35.415	70.994	1.00 24.30
ATOM	2904	CD2	LEU	A	369	4.014	35.728	73.384	1.00 21.81
ATOM	2905	N	THR	A	370	-0.577	33.154	73.953	1.00 30.26
ATOM	2906	CA	THR	A	370	-2.022	33.306	74.093	1.00 31.38
ATOM	2907	C	THR	A	370	-2.355	34.519	74.941	1.00 38.62
ATOM	2908	O	THR	A	370	-1.821	34.714	76.027	1.00 38.84
ATOM	2909	CB	THR	A	370	-2.601	32.056	74.750	1.00 34.04
ATOM	2910	OG1	THR	A	370	-2.472	30.949	73.873	1.00 29.99
ATOM	2911	CG2	THR	A	370	-4.091	32.266	75.052	1.00 26.40
ATOM	2912	N	ASP	A	371	-3.173	35.387	74.363	1.00 37.89
ATOM	2913	CA	ASP	A	371	-3.641	36.612	75.012	1.00 37.85

ATOM	2978	O	SER	A	379	14.100	39.334	72.843	1.00 18.46
ATOM	2979	CB	SER	A	379	12.976	39.740	76.067	1.00 23.56
ATOM	2980	OG	SER	A	379	12.805	38.329	75.883	1.00 37.26
ATOM	2981	N	SER	A	380	15.424	39.697	74.651	1.00 23.65
ATOM	2982	CA	SER	A	380	16.701	39.084	74.222	1.00 26.09
ATOM	2983	C	SER	A	380	16.669	37.571	74.457	1.00 28.37
ATOM	2984	O	SER	A	380	17.480	36.785	73.975	1.00 30.81
ATOM	2985	CB	SER	A	380	17.889	39.588	75.062	1.00 31.60
ATOM	2986	OG	SER	A	380	18.036	41.000	75.033	1.00 42.48
ATOM	2987	N	VAL	A	381	15.718	37.188	75.260	1.00 18.04
ATOM	2988	CA	VAL	A	381	15.595	35.812	75.598	1.00 14.91
ATOM	2989	C	VAL	A	381	15.708	34.897	74.419	1.00 20.31
ATOM	2990	O	VAL	A	381	16.620	34.091	74.330	1.00 27.64
ATOM	2991	CB	VAL	A	381	14.408	35.546	76.501	1.00 16.34
ATOM	2992	CG1	VAL	A	381	14.284	34.062	76.734	1.00 17.26
ATOM	2993	CG2	VAL	A	381	14.687	36.204	77.829	1.00 13.94
ATOM	2994	N	PRO	A	382	14.797	35.005	73.489	1.00 16.53
ATOM	2995	CA	PRO	A	382	14.886	34.139	72.324	1.00 17.21
ATOM	2996	C	PRO	A	382	16.222	34.230	71.634	1.00 24.01
ATOM	2997	O	PRO	A	382	16.709	33.192	71.207	1.00 27.79
ATOM	2998	CB	PRO	A	382	13.777	34.514	71.351	1.00 17.20
ATOM	2999	CG	PRO	A	382	13.003	35.618	72.033	1.00 18.32
ATOM	3000	CD	PRO	A	382	13.627	35.873	73.399	1.00 12.12
ATOM	3001	N	TYR	A	383	16.809	35.447	71.542	1.00 19.33
ATOM	3002	CA	TYR	A	383	18.112	35.648	70.902	1.00 19.70
ATOM	3003	C	TYR	A	383	19.246	34.953	71.651	1.00 28.79
ATOM	3004	O	TYR	A	383	19.980	34.117	71.104	1.00 31.38
ATOM	3005	CB	TYR	A	383	18.468	37.135	70.894	1.00 21.02
ATOM	3006	CG	TYR	A	383	17.593	37.968	70.011	1.00 23.86
ATOM	3007	CD1	TYR	A	383	16.290	38.277	70.404	1.00 28.36
ATOM	3008	CD2	TYR	A	383	18.067	38.450	68.784	1.00 20.93
ATOM	3009	CE1	TYR	A	383	15.473	39.054	69.576	1.00 30.88
ATOM	3010	CE2	TYR	A	383	17.272	39.244	67.957	1.00 18.71
ATOM	3011	CZ	TYR	A	383	15.967	39.533	68.358	1.00 25.95
ATOM	3012	OH	TYR	A	383	15.171	40.294	67.556	1.00 30.84
ATOM	3013	N	GLU	A	384	19.389	35.333	72.921	1.00 20.17
ATOM	3014	CA	GLU	A	384	20.419	34.857	73.803	1.00 17.57
ATOM	3015	C	GLU	A	384	20.188	33.506	74.405	1.00 22.88
ATOM	3016	O	GLU	A	384	21.151	32.775	74.669	1.00 25.65
ATOM	3017	CB	GLU	A	384	20.833	35.973	74.773	1.00 20.44
ATOM	3018	CG	GLU	A	384	21.263	37.202	73.944	1.00 15.21
ATOM	3019	CD	GLU	A	384	22.539	36.937	73.184	1.00 26.58
ATOM	3020	OE1	GLU	A	384	23.185	35.915	73.293	1.00 17.84
ATOM	3021	OE2	GLU	A	384	22.887	37.915	72.400	1.00 21.88
ATOM	3022	N	LYS	A	385	18.935	33.116	74.610	1.00 20.33
ATOM	3023	CA	LYS	A	385	18.736	31.767	75.146	1.00 20.05
ATOM	3024	C	LYS	A	385	18.865	30.716	74.028	1.00 27.19
ATOM	3025	O	LYS	A	385	19.420	29.621	74.219	1.00 31.66
ATOM	3026	CB	LYS	A	385	17.507	31.577	76.014	1.00 21.51
ATOM	3027	CG	LYS	A	385	17.676	30.384	76.953	1.00 22.29
ATOM	3028	CD	LYS	A	385	16.386	29.820	77.518	1.00 19.87
ATOM	3029	CE	LYS	A	385	16.049	30.277	78.937	1.00 31.60
ATOM	3030	NZ	LYS	A	385	14.783	29.694	79.441	1.00 30.38
ATOM	3031	N	GLY	A	386	18.364	31.084	72.832	1.00 20.72
ATOM	3032	CA	GLY	A	386	18.453	30.248	71.637	1.00 17.41
ATOM	3033	C	GLY	A	386	19.924	30.106	71.298	1.00 20.81
ATOM	3034	O	GLY	A	386	20.396	29.001	71.225	1.00 22.50
ATOM	3035	N	PHE	A	387	20.683	31.228	71.163	1.00 20.30
ATOM	3036	CA	PHE	A	387	22.137	31.158	70.900	1.00 19.92
ATOM	3037	C	PHE	A	387	22.840	30.263	71.905	1.00 29.09
ATOM	3038	O	PHE	A	387	23.685	29.478	71.530	1.00 32.80
ATOM	3039	CB	PHE	A	387	22.852	32.519	70.955	1.00 20.07
ATOM	3040	CG	PHE	A	387	24.344	32.358	70.872	1.00 19.41
ATOM	3041	CD1	PHE	A	387	24.949	32.163	69.631	1.00 19.67

ATOM	3042	CD2	PHE	A	387	25.157	32.373	72.007	1.00 25.27
ATOM	3043	CE1	PHE	A	387	26.329	31.977	69.525	1.00 20.88
ATOM	3044	CE2	PHE	A	387	26.542	32.202	71.916	1.00 28.83
ATOM	3045	CZ	PHE	A	387	27.131	31.981	70.668	1.00 23.24
ATOM	3046	N	ALA	A	388	22.495	30.381	73.203	1.00 25.48
ATOM	3047	CA	ALA	A	388	23.133	29.556	74.242	1.00 23.14
ATOM	3048	C	ALA	A	388	22.872	28.108	74.055	1.00 32.10
ATOM	3049	O	ALA	A	388	23.757	27.282	74.258	1.00 37.82
ATOM	3050	CB	ALA	A	388	22.717	29.932	75.633	1.00 23.02
ATOM	3051	N	LEU	A	389	21.636	27.793	73.691	1.00 26.31
ATOM	3052	CA	LEU	A	389	21.275	26.405	73.460	1.00 21.42
ATOM	3053	C	LEU	A	389	22.189	25.906	72.372	1.00 27.91
ATOM	3054	O	LEU	A	389	22.865	24.900	72.532	1.00 29.25
ATOM	3055	CB	LEU	A	389	19.841	26.300	72.937	1.00 19.24
ATOM	3056	CG	LEU	A	389	19.427	24.868	72.632	1.00 17.17
ATOM	3057	CD1	LEU	A	389	19.717	24.017	73.844	1.00 14.63
ATOM	3058	CD2	LEU	A	389	17.943	24.808	72.328	1.00 10.16
ATOM	3059	N	LEU	A	390	22.217	26.659	71.262	1.00 24.49
ATOM	3060	CA	LEU	A	390	23.050	26.340	70.107	1.00 25.05
ATOM	3061	C	LEU	A	390	24.531	26.256	70.383	1.00 32.31
ATOM	3062	O	LEU	A	390	25.183	25.301	69.932	1.00 33.60
ATOM	3063	CB	LEU	A	390	22.765	27.152	68.844	1.00 23.33
ATOM	3064	CG	LEU	A	390	21.307	27.026	68.442	1.00 23.38
ATOM	3065	CD1	LEU	A	390	20.986	28.025	67.334	1.00 20.84
ATOM	3066	CD2	LEU	A	390	20.988	25.591	68.017	1.00 18.86
ATOM	3067	N	PHE	A	391	25.058	27.231	71.127	1.00 28.52
ATOM	3068	CA	PHE	A	391	26.480	27.236	71.494	1.00 27.82
ATOM	3069	C	PHE	A	391	26.813	25.992	72.312	1.00 28.67
ATOM	3070	O	PHE	A	391	27.839	25.331	72.148	1.00 26.96
ATOM	3071	CB	PHE	A	391	26.834	28.455	72.341	1.00 28.60
ATOM	3072	CG	PHE	A	391	28.296	28.786	72.283	1.00 30.53
ATOM	3073	CD1	PHE	A	391	28.967	28.816	71.064	1.00 35.08
ATOM	3074	CD2	PHE	A	391	29.020	29.063	73.440	1.00 36.52
ATOM	3075	CE1	PHE	A	391	30.320	29.142	70.983	1.00 37.61
ATOM	3076	CE2	PHE	A	391	30.378	29.383	73.382	1.00 40.61
ATOM	3077	CZ	PHE	A	391	31.026	29.432	72.148	1.00 37.64
ATOM	3078	N	TYR	A	392	25.913	25.699	73.225	1.00 24.90
ATOM	3079	CA	TYR	A	392	26.044	24.550	74.065	1.00 24.66
ATOM	3080	C	TYR	A	392	26.106	23.298	73.186	1.00 34.30
ATOM	3081	O	TYR	A	392	27.058	22.558	73.268	1.00 37.51
ATOM	3082	CB	TYR	A	392	24.821	24.501	74.967	1.00 26.39
ATOM	3083	CG	TYR	A	392	24.631	23.181	75.678	1.00 31.99
ATOM	3084	CD1	TYR	A	392	25.546	22.715	76.625	1.00 35.17
ATOM	3085	CD2	TYR	A	392	23.501	22.397	75.432	1.00 32.49
ATOM	3086	CE1	TYR	A	392	25.341	21.512	77.306	1.00 39.01
ATOM	3087	CE2	TYR	A	392	23.281	21.184	76.094	1.00 31.50
ATOM	3088	CZ	TYR	A	392	24.206	20.743	77.035	1.00 34.08
ATOM	3089	OH	TYR	A	392	23.986	19.564	77.683	1.00 36.46
ATOM	3090	N	LEU	A	393	25.101	23.067	72.310	1.00 31.02
ATOM	3091	CA	LEU	A	393	25.043	21.889	71.410	1.00 29.65
ATOM	3092	C	LEU	A	393	26.274	21.616	70.507	1.00 32.03
ATOM	3093	O	LEU	A	393	26.664	20.468	70.267	1.00 27.90
ATOM	3094	CB	LEU	A	393	23.758	21.905	70.552	1.00 28.85
ATOM	3095	CG	LEU	A	393	22.489	21.688	71.375	1.00 30.33
ATOM	3096	CD1	LEU	A	393	21.256	22.047	70.559	1.00 27.38
ATOM	3097	CD2	LEU	A	393	22.400	20.246	71.865	1.00 29.76
ATOM	3098	N	GLU	A	394	26.841	22.701	69.980	1.00 30.84
ATOM	3099	CA	GLU	A	394	28.000	22.727	69.118	1.00 30.05
ATOM	3100	C	GLU	A	394	29.210	22.214	69.868	1.00 39.16
ATOM	3101	O	GLU	A	394	30.089	21.595	69.299	1.00 42.14
ATOM	3102	CB	GLU	A	394	28.300	24.204	68.756	1.00 31.03
ATOM	3103	CG	GLU	A	394	29.776	24.406	68.376	1.00 37.11
ATOM	3104	CD	GLU	A	394	30.182	25.830	68.208	1.00 45.20
ATOM	3105	OE1	GLU	A	394	29.614	26.609	67.471	1.00 56.77

ATOM	3106	OE2	GLU	A	394	31.229	26.133	68.927	1.00 39.77
ATOM	3107	N	GLN	A	395	29.256	22.534	71.160	1.00 34.20
ATOM	3108	CA	GLN	A	395	30.342	22.139	72.029	1.00 32.86
ATOM	3109	C	GLN	A	395	30.143	20.690	72.435	1.00 38.65
ATOM	3110	O	GLN	A	395	31.066	19.899	72.507	1.00 38.67
ATOM	3111	CB	GLN	A	395	30.474	23.051	73.287	1.00 33.17
ATOM	3112	CG	GLN	A	395	30.831	24.540	72.996	1.00 13.79
ATOM	3113	CD	GLN	A	395	31.176	25.354	74.247	1.00 37.45
ATOM	3114	OE1	GLN	A	395	30.909	24.959	75.407	1.00 26.89
ATOM	3115	NE2	GLN	A	395	31.758	26.523	74.010	1.00 31.99
ATOM	3116	N	LEU	A	396	28.903	20.352	72.682	1.00 38.68
ATOM	3117	CA	LEU	A	396	28.514	19.015	73.083	1.00 38.49
ATOM	3118	C	LEU	A	396	28.633	18.017	71.924	1.00 39.28
ATOM	3119	O	LEU	A	396	29.012	16.871	72.100	1.00 42.17
ATOM	3120	CB	LEU	A	396	27.055	19.072	73.628	1.00 37.93
ATOM	3121	CG	LEU	A	396	26.389	17.732	73.946	1.00 42.72
ATOM	3122	CD1	LEU	A	396	26.436	17.489	75.445	1.00 45.42
ATOM	3123	CD2	LEU	A	396	24.917	17.709	73.527	1.00 43.81
ATOM	3124	N	LEU	A	397	28.303	18.456	70.730	1.00 28.48
ATOM	3125	CA	LEU	A	397	28.337	17.595	69.589	1.00 25.49
ATOM	3126	C	LEU	A	397	29.620	17.609	68.771	1.00 36.86
ATOM	3127	O	LEU	A	397	29.596	17.220	67.599	1.00 39.85
ATOM	3128	CB	LEU	A	397	27.156	17.924	68.686	1.00 23.73
ATOM	3129	CG	LEU	A	397	25.843	17.773	69.401	1.00 25.82
ATOM	3130	CD1	LEU	A	397	24.740	18.559	68.669	1.00 22.99
ATOM	3131	CD2	LEU	A	397	25.525	16.272	69.452	1.00 27.30
ATOM	3132	N	GLY	A	398	30.731	18.069	69.342	1.00 33.98
ATOM	3133	CA	GLY	A	398	31.993	18.038	68.617	1.00 34.14
ATOM	3134	C	GLY	A	398	32.547	19.260	67.889	1.00 38.92
ATOM	3135	O	GLY	A	398	33.502	19.097	67.115	1.00 39.98
ATOM	3136	N	GLY	A	399	32.001	20.457	68.105	1.00 33.01
ATOM	3137	CA	GLY	A	399	32.543	21.650	67.440	1.00 30.35
ATOM	3138	C	GLY	A	399	31.713	22.336	66.365	1.00 31.72
ATOM	3139	O	GLY	A	399	30.800	21.823	65.762	1.00 34.57
ATOM	3140	N	PRO	A	400	32.076	23.550	66.124	1.00 33.01
ATOM	3141	CA	PRO	A	400	31.429	24.406	65.151	1.00 35.02
ATOM	3142	C	PRO	A	400	31.379	23.794	63.750	1.00 43.93
ATOM	3143	O	PRO	A	400	30.360	23.838	63.045	1.00 40.14
ATOM	3144	CB	PRO	A	400	32.293	25.672	65.111	1.00 35.73
ATOM	3145	CG	PRO	A	400	33.539	25.411	65.948	1.00 38.03
ATOM	3146	CD	PRO	A	400	33.423	24.010	66.517	1.00 33.92
ATOM	3147	N	GLU	A	401	32.512	23.237	63.345	1.00 43.85
ATOM	3148	CA	GLU	A	401	32.597	22.620	62.042	1.00 42.92
ATOM	3149	C	GLU	A	401	31.491	21.587	61.878	1.00 37.92
ATOM	3150	O	GLU	A	401	30.810	21.588	60.866	1.00 33.79
ATOM	3151	CB	GLU	A	401	33.996	22.034	61.789	1.00 45.93
ATOM	3152	CG	GLU	A	401	34.578	22.372	60.398	1.00 69.62
ATOM	3153	CD	GLU	A	401	35.603	21.373	59.911	1.00100.00
ATOM	3154	OE1	GLU	A	401	36.702	21.236	60.427	1.00100.00
ATOM	3155	OE2	GLU	A	401	35.195	20.689	58.865	1.00 93.16
ATOM	3156	N	ILE	A	402	31.317	20.720	62.902	1.00 34.58
ATOM	3157	CA	ILE	A	402	30.281	19.681	62.922	1.00 33.20
ATOM	3158	C	ILE	A	402	28.898	20.291	62.938	1.00 39.09
ATOM	3159	O	ILE	A	402	28.065	19.896	62.133	1.00 41.43
ATOM	3160	CB	ILE	A	402	30.391	18.673	64.078	1.00 33.82
ATOM	3161	CG1	ILE	A	402	31.490	17.661	63.811	1.00 34.70
ATOM	3162	CG2	ILE	A	402	29.080	17.900	64.287	1.00 23.32
ATOM	3163	CD1	ILE	A	402	31.878	16.896	65.080	1.00 49.20
ATOM	3164	N	PHE	A	403	28.668	21.246	63.868	1.00 32.73
ATOM	3165	CA	PHE	A	403	27.390	21.952	64.044	1.00 29.52
ATOM	3166	C	PHE	A	403	27.032	22.816	62.836	1.00 33.94
ATOM	3167	O	PHE	A	403	25.866	23.022	62.469	1.00 34.15
ATOM	3168	CB	PHE	A	403	27.319	22.719	65.381	1.00 29.03
ATOM	3169	CG	PHE	A	403	25.917	22.783	65.929	1.00 28.54

ATOM	3170	CD1	PHE	A	403	25.323	21.643	66.484	1.00 29.91
ATOM	3171	CD2	PHE	A	403	25.176	23.964	65.873	1.00 27.62
ATOM	3172	CE1	PHE	A	403	24.021	21.667	66.990	1.00 27.38
ATOM	3173	CE2	PHE	A	403	23.881	24.017	66.393	1.00 28.82
ATOM	3174	CZ	PHE	A	403	23.304	22.863	66.932	1.00 25.72
ATOM	3175	N	LEU	A	404	28.040	23.327	62.165	1.00 31.31
ATOM	3176	CA	LEU	A	404	27.687	24.080	60.983	1.00 32.95
ATOM	3177	C	LEU	A	404	27.068	23.099	59.952	1.00 32.89
ATOM	3178	O	LEU	A	404	26.050	23.361	59.315	1.00 37.36
ATOM	3179	CB	LEU	A	404	28.798	25.045	60.464	1.00 33.15
ATOM	3180	CG	LEU	A	404	29.029	26.208	61.444	1.00 36.96
ATOM	3181	CD1	LEU	A	404	30.454	26.717	61.353	1.00 37.13
ATOM	3182	CD2	LEU	A	404	28.083	27.362	61.163	1.00 39.27
ATOM	3183	N	GLY	A	405	27.670	21.921	59.826	1.00 22.02
ATOM	3184	CA	GLY	A	405	27.167	20.908	58.928	1.00 22.77
ATOM	3185	C	GLY	A	405	25.698	20.676	59.206	1.00 31.85
ATOM	3186	O	GLY	A	405	24.885	20.438	58.297	1.00 33.01
ATOM	3187	N	PHE	A	406	25.364	20.747	60.493	1.00 26.28
ATOM	3188	CA	PHE	A	406	23.992	20.565	60.863	1.00 25.27
ATOM	3189	C	PHE	A	406	23.188	21.757	60.365	1.00 34.80
ATOM	3190	O	PHE	A	406	22.195	21.629	59.638	1.00 36.22
ATOM	3191	CB	PHE	A	406	23.798	20.268	62.351	1.00 24.52
ATOM	3192	CG	PHE	A	406	22.388	20.525	62.798	1.00 24.82
ATOM	3193	CD1	PHE	A	406	21.328	19.734	62.353	1.00 28.50
ATOM	3194	CD2	PHE	A	406	22.107	21.579	63.669	1.00 30.12
ATOM	3195	CE1	PHE	A	406	20.025	19.977	62.793	1.00 31.40
ATOM	3196	CE2	PHE	A	406	20.810	21.862	64.105	1.00 32.57
ATOM	3197	CZ	PHE	A	406	19.771	21.037	63.669	1.00 31.88
ATOM	3198	N	LEU	A	407	23.661	22.934	60.708	1.00 32.11
ATOM	3199	CA	LEU	A	407	22.972	24.132	60.269	1.00 33.11
ATOM	3200	C	LEU	A	407	22.706	24.204	58.767	1.00 34.74
ATOM	3201	O	LEU	A	407	21.635	24.615	58.341	1.00 35.21
ATOM	3202	CB	LEU	A	407	23.589	25.420	60.840	1.00 35.36
ATOM	3203	CG	LEU	A	407	22.597	26.577	60.855	1.00 41.79
ATOM	3204	CD1	LEU	A	407	23.048	27.626	61.833	1.00 40.45
ATOM	3205	CD2	LEU	A	407	22.513	27.197	59.461	1.00 49.57
ATOM	3206	N	LYS	A	408	23.667	23.804	57.948	1.00 34.92
ATOM	3207	CA	LYS	A	408	23.476	23.826	56.490	1.00 36.29
ATOM	3208	C	LYS	A	408	22.378	22.876	56.037	1.00 38.15
ATOM	3209	O	LYS	A	408	21.568	23.191	55.160	1.00 35.09
ATOM	3210	CB	LYS	A	408	24.747	23.517	55.707	1.00 40.54
ATOM	3211	CG	LYS	A	408	24.633	23.873	54.214	1.00 43.41
ATOM	3212	CD	LYS	A	408	25.950	23.796	53.422	1.00 49.26
ATOM	3213	CE	LYS	A	408	26.808	25.059	53.459	1.00 61.45
ATOM	3214	NZ	LYS	A	408	28.014	24.994	52.606	1.00 73.78
ATOM	3215	N	ALA	A	409	22.352	21.690	56.655	1.00 35.34
ATOM	3216	CA	ALA	A	409	21.333	20.698	56.298	1.00 36.14
ATOM	3217	C	ALA	A	409	19.927	21.041	56.814	1.00 38.45
ATOM	3218	O	ALA	A	409	18.913	20.821	56.134	1.00 37.39
ATOM	3219	CB	ALA	A	409	21.762	19.273	56.626	1.00 36.66
ATOM	3220	N	TYR	A	410	19.902	21.597	58.030	1.00 33.14
ATOM	3221	CA	TYR	A	410	18.693	22.059	58.682	1.00 29.65
ATOM	3222	C	TYR	A	410	18.028	23.051	57.730	1.00 35.55
ATOM	3223	O	TYR	A	410	16.855	22.976	57.399	1.00 37.26
ATOM	3224	CB	TYR	A	410	19.117	22.762	59.970	1.00 24.67
ATOM	3225	CG	TYR	A	410	18.069	23.643	60.541	1.00 26.95
ATOM	3226	CD1	TYR	A	410	16.861	23.112	60.990	1.00 28.10
ATOM	3227	CD2	TYR	A	410	18.288	25.015	60.663	1.00 29.66
ATOM	3228	CE1	TYR	A	410	15.883	23.924	61.571	1.00 26.98
ATOM	3229	CE2	TYR	A	410	17.316	25.839	61.230	1.00 31.84
ATOM	3230	CZ	TYR	A	410	16.112	25.294	61.685	1.00 37.49
ATOM	3231	OH	TYR	A	410	15.156	26.110	62.241	1.00 33.48
ATOM	3232	N	VAL	A	411	18.848	23.961	57.262	1.00 28.75
ATOM	3233	CA	VAL	A	411	18.457	24.984	56.341	1.00 29.23

ATOM	3234	C	VAL	A	411	18.013	24.469	54.992	1.00 34.00
ATOM	3235	O	VAL	A	411	17.060	24.982	54.401	1.00 30.00
ATOM	3236	CB	VAL	A	411	19.617	25.922	56.139	1.00 32.22
ATOM	3237	CG1	VAL	A	411	19.331	26.821	54.950	1.00 29.86
ATOM	3238	CG2	VAL	A	411	19.850	26.708	57.431	1.00 31.69
ATOM	3239	N	GLU	A	412	18.730	23.479	54.488	1.00 33.14
ATOM	3240	CA	GLU	A	412	18.402	22.900	53.217	1.00 31.91
ATOM	3241	C	GLU	A	412	17.068	22.163	53.355	1.00 30.32
ATOM	3242	O	GLU	A	412	16.182	22.225	52.531	1.00 31.89
ATOM	3243	CB	GLU	A	412	19.502	21.883	52.932	1.00 36.48
ATOM	3244	CG	GLU	A	412	20.443	22.174	51.737	1.00 67.01
ATOM	3245	CD	GLU	A	412	21.872	21.699	51.962	1.00100.00
ATOM	3246	OE1	GLU	A	412	22.193	20.782	52.716	1.00100.00
ATOM	3247	OE2	GLU	A	412	22.750	22.396	51.277	1.00 94.73
ATOM	3248	N	LYS	A	413	16.922	21.444	54.444	1.00 22.18
ATOM	3249	CA	LYS	A	413	15.729	20.692	54.714	1.00 17.91
ATOM	3250	C	LYS	A	413	14.463	21.486	54.855	1.00 23.75
ATOM	3251	O	LYS	A	413	13.417	20.978	54.503	1.00 25.92
ATOM	3252	CB	LYS	A	413	15.890	19.911	55.988	1.00 15.65
ATOM	3253	CG	LYS	A	413	14.554	19.422	56.503	1.00 38.69
ATOM	3254	CD	LYS	A	413	14.150	18.089	55.903	1.00 58.11
ATOM	3255	CE	LYS	A	413	13.634	17.099	56.937	1.00 64.98
ATOM	3256	NZ	LYS	A	413	13.457	15.751	56.381	1.00 73.89
ATOM	3257	N	PHE	A	414	14.530	22.688	55.424	1.00 25.40
ATOM	3258	CA	PHE	A	414	13.316	23.479	55.640	1.00 27.80
ATOM	3259	C	PHE	A	414	13.151	24.748	54.821	1.00 35.82
ATOM	3260	O	PHE	A	414	12.276	25.557	55.122	1.00 35.17
ATOM	3261	CB	PHE	A	414	13.063	23.791	57.118	1.00 30.46
ATOM	3262	CG	PHE	A	414	12.936	22.553	57.964	1.00 33.88
ATOM	3263	CD1	PHE	A	414	11.746	21.826	57.996	1.00 35.94
ATOM	3264	CD2	PHE	A	414	14.005	22.110	58.742	1.00 37.75
ATOM	3265	CE1	PHE	A	414	11.629	20.664	58.761	1.00 37.77
ATOM	3266	CE2	PHE	A	414	13.888	20.962	59.526	1.00 42.23
ATOM	3267	CZ	PHE	A	414	12.698	20.231	59.542	1.00 39.10
ATOM	3268	N	SER	A	415	13.970	24.933	53.795	1.00 36.12
ATOM	3269	CA	SER	A	415	13.858	26.115	52.945	1.00 36.36
ATOM	3270	C	SER	A	415	12.412	26.295	52.510	1.00 38.99
ATOM	3271	O	SER	A	415	11.730	25.315	52.243	1.00 41.04
ATOM	3272	CB	SER	A	415	14.773	26.008	51.736	1.00 37.43
ATOM	3273	OG	SER	A	415	16.036	26.566	52.046	1.00 46.73
ATOM	3274	N	TYR	A	416	11.928	27.537	52.475	1.00 33.40
ATOM	3275	CA	TYR	A	416	10.541	27.832	52.072	1.00 30.88
ATOM	3276	C	TYR	A	416	9.453	27.183	52.947	1.00 33.62
ATOM	3277	O	TYR	A	416	8.295	27.095	52.546	1.00 33.44
ATOM	3278	CB	TYR	A	416	10.292	27.479	50.584	1.00 28.42
ATOM	3279	CG	TYR	A	416	11.496	27.782	49.723	1.00 24.76
ATOM	3280	CD1	TYR	A	416	11.791	29.087	49.338	1.00 26.55
ATOM	3281	CD2	TYR	A	416	12.375	26.778	49.335	1.00 21.68
ATOM	3282	CE1	TYR	A	416	12.914	29.384	48.570	1.00 25.16
ATOM	3283	CE2	TYR	A	416	13.504	27.052	48.572	1.00 20.15
ATOM	3284	CZ	TYR	A	416	13.780	28.360	48.189	1.00 30.62
ATOM	3285	OH	TYR	A	416	14.892	28.616	47.399	1.00 35.15
ATOM	3286	N	LYS	A	417	9.823	26.713	54.122	1.00 27.67
ATOM	3287	CA	LYS	A	417	8.889	26.065	55.008	1.00 28.02
ATOM	3288	C	LYS	A	417	8.733	26.830	56.317	1.00 31.36
ATOM	3289	O	LYS	A	417	9.547	27.671	56.682	1.00 33.15
ATOM	3290	CB	LYS	A	417	9.335	24.615	55.252	1.00 33.86
ATOM	3291	CG	LYS	A	417	8.449	23.792	56.201	1.00 86.28
ATOM	3292	CD	LYS	A	417	8.742	22.275	56.232	1.00100.00
ATOM	3293	CE	LYS	A	417	7.924	21.471	57.265	1.00 72.28
ATOM	3294	NZ	LYS	A	417	8.280	20.033	57.323	1.00 41.88
ATOM	3295	N	SER	A	418	7.668	26.557	57.033	1.00 28.88
ATOM	3296	CA	SER	A	418	7.455	27.195	58.335	1.00 30.04
ATOM	3297	C	SER	A	418	7.425	26.064	59.332	1.00 34.09

ATOM	3298	O	SER	A	418	6.614	25.145	59.193	1.00 31.54
ATOM	3299	CB	SER	A	418	6.261	28.126	58.410	1.00 31.46
ATOM	3300	OG	SER	A	418	6.417	29.106	57.399	1.00 35.01
ATOM	3301	N	ILE	A	419	8.356	26.077	60.281	1.00 28.50
ATOM	3302	CA	ILE	A	419	8.446	24.971	61.205	1.00 23.86
ATOM	3303	C	ILE	A	419	8.272	25.342	62.641	1.00 25.06
ATOM	3304	O	ILE	A	419	8.122	26.500	63.002	1.00 21.64
ATOM	3305	CB	ILE	A	419	9.803	24.314	61.026	1.00 25.02
ATOM	3306	CG1	ILE	A	419	10.863	25.325	61.399	1.00 23.63
ATOM	3307	CG2	ILE	A	419	10.051	23.937	59.565	1.00 23.22
ATOM	3308	CD1	ILE	A	419	12.236	24.688	61.253	1.00 23.48
ATOM	3309	N	THR	A	420	8.321	24.302	63.455	1.00 24.71
ATOM	3310	CA	THR	A	420	8.201	24.417	64.895	1.00 24.36
ATOM	3311	C	THR	A	420	9.416	23.795	65.538	1.00 28.90
ATOM	3312	O	THR	A	420	10.190	23.112	64.863	1.00 23.38
ATOM	3313	CB	THR	A	420	6.979	23.691	65.448	1.00 24.92
ATOM	3314	OG1	THR	A	420	7.190	22.313	65.291	1.00 26.43
ATOM	3315	CG2	THR	A	420	5.728	24.082	64.694	1.00 31.57
ATOM	3316	N	THR	A	421	9.542	24.051	66.855	1.00 29.30
ATOM	3317	CA	THR	A	421	10.610	23.549	67.709	1.00 27.78
ATOM	3318	C	THR	A	421	10.831	22.035	67.585	1.00 30.99
ATOM	3319	O	THR	A	421	11.975	21.594	67.489	1.00 33.28
ATOM	3320	CB	THR	A	421	10.394	23.969	69.166	1.00 21.94
ATOM	3321	OG1	THR	A	421	10.567	25.369	69.263	1.00 24.52
ATOM	3322	CG2	THR	A	421	11.399	23.221	70.045	1.00 20.12
ATOM	3323	N	ASP	A	422	9.721	21.272	67.575	1.00 21.94
ATOM	3324	CA	ASP	A	422	9.706	19.823	67.430	1.00 21.08
ATOM	3325	C	ASP	A	422	10.323	19.401	66.104	1.00 31.16
ATOM	3326	O	ASP	A	422	11.110	18.427	66.027	1.00 31.95
ATOM	3327	CB	ASP	A	422	8.276	19.278	67.561	1.00 19.49
ATOM	3328	CG	ASP	A	422	8.236	17.802	67.298	1.00 31.85
ATOM	3329	OD1	ASP	A	422	9.130	17.040	67.654	1.00 29.73
ATOM	3330	OD2	ASP	A	422	7.197	17.415	66.598	1.00 56.60
ATOM	3331	N	ASP	A	423	9.957	20.146	65.049	1.00 26.75
ATOM	3332	CA	ASP	A	423	10.505	19.876	63.729	1.00 26.01
ATOM	3333	C	ASP	A	423	12.027	19.957	63.830	1.00 40.09
ATOM	3334	O	ASP	A	423	12.753	19.020	63.500	1.00 47.09
ATOM	3335	CB	ASP	A	423	10.000	20.833	62.631	1.00 24.86
ATOM	3336	CG	ASP	A	423	8.538	20.722	62.343	1.00 39.90
ATOM	3337	OD1	ASP	A	423	7.968	19.649	62.299	1.00 45.03
ATOM	3338	OD2	ASP	A	423	7.943	21.887	62.113	1.00 40.43
ATOM	3339	N	TRP	A	424	12.493	21.099	64.320	1.00 31.92
ATOM	3340	CA	TRP	A	424	13.903	21.372	64.495	1.00 29.69
ATOM	3341	C	TRP	A	424	14.611	20.271	65.282	1.00 33.81
ATOM	3342	O	TRP	A	424	15.537	19.616	64.824	1.00 35.87
ATOM	3343	CB	TRP	A	424	14.056	22.711	65.239	1.00 26.11
ATOM	3344	CG	TRP	A	424	15.431	22.869	65.786	1.00 27.05
ATOM	3345	CD1	TRP	A	424	16.518	23.302	65.101	1.00 29.65
ATOM	3346	CD2	TRP	A	424	15.885	22.587	67.119	1.00 26.62
ATOM	3347	NE1	TRP	A	424	17.612	23.321	65.922	1.00 27.83
ATOM	3348	CE2	TRP	A	424	17.257	22.891	67.163	1.00 28.62
ATOM	3349	CE3	TRP	A	424	15.260	22.138	68.269	1.00 29.69
ATOM	3350	CZ2	TRP	A	424	18.010	22.758	68.319	1.00 29.28
ATOM	3351	CZ3	TRP	A	424	16.000	21.993	69.429	1.00 33.50
ATOM	3352	CH2	TRP	A	424	17.362	22.317	69.459	1.00 33.93
ATOM	3353	N	LYS	A	425	14.156	20.090	66.497	1.00 28.75
ATOM	3354	CA	LYS	A	425	14.723	19.105	67.373	1.00 29.43
ATOM	3355	C	LYS	A	425	14.697	17.691	66.808	1.00 29.49
ATOM	3356	O	LYS	A	425	15.627	16.928	67.030	1.00 27.65
ATOM	3357	CB	LYS	A	425	14.078	19.171	68.744	1.00 29.70
ATOM	3358	CG	LYS	A	425	14.860	18.414	69.787	1.00 28.11
ATOM	3359	CD	LYS	A	425	14.161	18.409	71.132	1.00 23.57
ATOM	3360	CE	LYS	A	425	14.300	17.063	71.815	1.00 36.16
ATOM	3361	NZ	LYS	A	425	13.042	16.302	71.768	1.00 58.08

ATOM	3362	N	ASP	A	426	13.606	17.361	66.107	1.00 19.05
ATOM	3363	CA	ASP	A	426	13.417	16.070	65.516	1.00 18.43
ATOM	3364	C	ASP	A	426	14.453	15.879	64.387	1.00 28.33
ATOM	3365	O	ASP	A	426	15.070	14.832	64.232	1.00 31.25
ATOM	3366	CB	ASP	A	426	11.920	15.840	65.098	1.00 19.79
ATOM	3367	CG	ASP	A	426	10.998	15.575	66.274	1.00 25.54
ATOM	3368	OD1	ASP	A	426	11.341	15.466	67.409	1.00 29.73
ATOM	3369	OD2	ASP	A	426	9.804	15.611	65.938	1.00 20.67
ATOM	3370	N	PHE	A	427	14.674	16.926	63.612	1.00 25.09
ATOM	3371	CA	PHE	A	427	15.654	16.899	62.540	1.00 25.81
ATOM	3372	C	PHE	A	427	17.066	16.718	63.159	1.00 34.01
ATOM	3373	O	PHE	A	427	17.843	15.851	62.773	1.00 36.25
ATOM	3374	CB	PHE	A	427	15.589	18.197	61.704	1.00 26.35
ATOM	3375	CG	PHE	A	427	16.698	18.202	60.702	1.00 27.40
ATOM	3376	CD1	PHE	A	427	16.714	17.247	59.686	1.00 29.97
ATOM	3377	CD2	PHE	A	427	17.773	19.084	60.805	1.00 28.71
ATOM	3378	CE1	PHE	A	427	17.730	17.194	58.733	1.00 27.72
ATOM	3379	CE2	PHE	A	427	18.806	19.046	59.867	1.00 30.37
ATOM	3380	CZ	PHE	A	427	18.780	18.104	58.837	1.00 26.34
ATOM	3381	N	LEU	A	428	17.369	17.544	64.160	1.00 28.94
ATOM	3382	CA	LEU	A	428	18.622	17.496	64.924	1.00 27.74
ATOM	3383	C	LEU	A	428	18.989	16.047	65.303	1.00 32.08
ATOM	3384	O	LEU	A	428	20.145	15.647	65.209	1.00 36.38
ATOM	3385	CB	LEU	A	428	18.510	18.362	66.223	1.00 24.68
ATOM	3386	CG	LEU	A	428	19.778	18.377	67.079	1.00 24.30
ATOM	3387	CD1	LEU	A	428	20.855	19.278	66.467	1.00 23.00
ATOM	3388	CD2	LEU	A	428	19.446	18.856	68.481	1.00 16.41
ATOM	3389	N	TYR	A	429	17.991	15.271	65.735	1.00 23.71
ATOM	3390	CA	TYR	A	429	18.148	13.896	66.144	1.00 23.18
ATOM	3391	C	TYR	A	429	18.311	12.967	64.976	1.00 26.62
ATOM	3392	O	TYR	A	429	18.911	11.910	65.076	1.00 28.43
ATOM	3393	CB	TYR	A	429	16.921	13.453	66.914	1.00 25.59
ATOM	3394	CG	TYR	A	429	17.069	13.526	68.414	1.00 29.53
ATOM	3395	CD1	TYR	A	429	16.823	14.714	69.114	1.00 31.11
ATOM	3396	CD2	TYR	A	429	17.361	12.383	69.156	1.00 32.70
ATOM	3397	CE1	TYR	A	429	16.916	14.769	70.510	1.00 32.23
ATOM	3398	CE2	TYR	A	429	17.485	12.420	70.551	1.00 35.30
ATOM	3399	CZ	TYR	A	429	17.251	13.623	71.231	1.00 41.02
ATOM	3400	OH	TYR	A	429	17.339	13.679	72.609	1.00 30.02
ATOM	3401	N	SER	A	430	17.748	13.342	63.854	1.00 21.68
ATOM	3402	CA	SER	A	430	17.914	12.469	62.730	1.00 23.42
ATOM	3403	C	SER	A	430	19.264	12.722	62.050	1.00 32.87
ATOM	3404	O	SER	A	430	19.879	11.819	61.467	1.00 35.11
ATOM	3405	CB	SER	A	430	16.756	12.541	61.773	1.00 28.79
ATOM	3406	OG	SER	A	430	17.089	13.475	60.777	1.00 49.56
ATOM	3407	N	TYR	A	431	19.748	13.955	62.132	1.00 27.18
ATOM	3408	CA	TYR	A	431	21.017	14.296	61.537	1.00 27.14
ATOM	3409	C	TYR	A	431	22.152	13.702	62.316	1.00 32.52
ATOM	3410	O	TYR	A	431	23.155	13.242	61.771	1.00 33.64
ATOM	3411	CB	TYR	A	431	21.216	15.818	61.385	1.00 31.07
ATOM	3412	CG	TYR	A	431	22.566	16.265	60.812	1.00 35.63
ATOM	3413	CD1	TYR	A	431	23.663	16.492	61.650	1.00 36.88
ATOM	3414	CD2	TYR	A	431	22.735	16.496	59.444	1.00 36.92
ATOM	3415	CE1	TYR	A	431	24.894	16.924	61.157	1.00 33.78
ATOM	3416	CE2	TYR	A	431	23.964	16.916	58.924	1.00 37.86
ATOM	3417	CZ	TYR	A	431	25.038	17.143	59.786	1.00 46.01
ATOM	3418	OH	TYR	A	431	26.247	17.573	59.294	1.00 51.28
ATOM	3419	N	PHE	A	432	21.964	13.728	63.606	1.00 29.66
ATOM	3420	CA	PHE	A	432	22.939	13.215	64.526	1.00 29.12
ATOM	3421	C	PHE	A	432	22.522	11.865	65.007	1.00 42.64
ATOM	3422	O	PHE	A	432	22.499	11.593	66.197	1.00 46.77
ATOM	3423	CB	PHE	A	432	23.063	14.157	65.719	1.00 30.24
ATOM	3424	CG	PHE	A	432	23.962	15.327	65.401	1.00 33.03
ATOM	3425	CD1	PHE	A	432	25.336	15.113	65.277	1.00 37.22

ATOM	3426	CD2	PHE	A	432	23.470	16.624	65.232	1.00 30.70
ATOM	3427	CE1	PHE	A	432	26.223	16.153	64.999	1.00 34.27
ATOM	3428	CE2	PHE	A	432	24.349	17.667	64.938	1.00 31.71
ATOM	3429	CZ	PHE	A	432	25.722	17.438	64.823	1.00 27.82
ATOM	3430	N	LYS	A	433	22.174	11.029	64.063	1.00 42.50
ATOM	3431	CA	LYS	A	433	21.669	9.670	64.270	1.00 40.87
ATOM	3432	C	LYS	A	433	22.718	8.751	64.908	1.00 46.17
ATOM	3433	O	LYS	A	433	22.405	7.734	65.513	1.00 48.48
ATOM	3434	CB	LYS	A	433	21.245	9.106	62.917	1.00 39.25
ATOM	3435	CG	LYS	A	433	19.988	8.241	63.017	1.00 84.17
ATOM	3436	CD	LYS	A	433	18.925	8.660	62.000	1.00100.00
ATOM	3437	CE	LYS	A	433	17.523	8.172	62.384	1.00100.00
ATOM	3438	NZ	LYS	A	433	16.525	9.119	61.884	1.00100.00
ATOM	3439	N	ASP	A	434	24.002	9.112	64.697	1.00 45.20
ATOM	3440	CA	ASP	A	434	25.083	8.349	65.321	1.00 47.80
ATOM	3441	C	ASP	A	434	25.201	8.684	66.802	1.00 50.78
ATOM	3442	O	ASP	A	434	25.474	7.845	67.653	1.00 55.76
ATOM	3443	CB	ASP	A	434	26.405	8.567	64.562	1.00 53.91
ATOM	3444	CG	ASP	A	434	26.123	8.474	63.069	1.00 93.32
ATOM	3445	OD1	ASP	A	434	25.744	7.573	62.325	1.00 96.22
ATOM	3446	OD2	ASP	A	434	26.119	9.664	62.753	1.00100.00
ATOM	3447	N	LYS	A	435	25.015	9.978	67.085	1.00 38.82
ATOM	3448	CA	LYS	A	435	24.974	10.404	68.468	1.00 34.57
ATOM	3449	C	LYS	A	435	23.549	10.749	68.881	1.00 39.87
ATOM	3450	O	LYS	A	435	23.070	11.840	68.693	1.00 40.34
ATOM	3451	CB	LYS	A	435	25.864	11.631	68.615	1.00 34.69
ATOM	3452	CG	LYS	A	435	27.064	11.595	67.679	1.00 40.86
ATOM	3453	CD	LYS	A	435	27.703	12.975	67.532	1.00 51.04
ATOM	3454	CE	LYS	A	435	29.242	12.904	67.557	1.00 24.08
ATOM	3455	NZ	LYS	A	435	29.822	13.990	66.760	1.00 45.26
ATOM	3456	N	VAL	A	436	22.843	9.728	69.414	1.00 38.07
ATOM	3457	CA	VAL	A	436	21.601	10.036	70.111	1.00 36.86
ATOM	3458	C	VAL	A	436	21.846	10.129	71.608	1.00 44.88
ATOM	3459	O	VAL	A	436	21.289	10.948	72.300	1.00 46.42
ATOM	3460	CB	VAL	A	436	20.567	8.923	69.816	1.00 37.37
ATOM	3461	CG1	VAL	A	436	19.944	9.143	68.446	1.00 36.24
ATOM	3462	CG2	VAL	A	436	21.227	7.556	69.854	1.00 36.80
ATOM	3463	N	ASP	A	437	22.718	9.232	72.099	1.00 43.61
ATOM	3464	CA	ASP	A	437	23.044	9.222	73.522	1.00 41.43
ATOM	3465	C	ASP	A	437	23.657	10.546	73.958	1.00 45.71
ATOM	3466	O	ASP	A	437	23.554	10.956	75.107	1.00 49.89
ATOM	3467	CB	ASP	A	437	24.022	8.082	73.776	1.00 43.84
ATOM	3468	CG	ASP	A	437	23.281	6.752	73.691	1.00 72.47
ATOM	3469	OD1	ASP	A	437	22.062	6.769	73.823	1.00 74.64
ATOM	3470	OD2	ASP	A	437	23.933	5.730	73.481	1.00 86.09
ATOM	3471	N	VAL	A	438	24.333	11.324	73.122	1.00 40.21
ATOM	3472	CA	VAL	A	438	24.807	12.624	73.577	1.00 40.97
ATOM	3473	C	VAL	A	438	23.621	13.582	73.668	1.00 41.86
ATOM	3474	O	VAL	A	438	23.368	14.276	74.657	1.00 39.95
ATOM	3475	CB	VAL	A	438	25.875	13.165	72.615	1.00 47.47
ATOM	3476	CG1	VAL	A	438	26.438	14.523	73.051	1.00 47.51
ATOM	3477	CG2	VAL	A	438	26.996	12.149	72.440	1.00 47.51
ATOM	3478	N	LEU	A	439	22.876	13.595	72.585	1.00 37.91
ATOM	3479	CA	LEU	A	439	21.729	14.442	72.507	1.00 36.21
ATOM	3480	C	LEU	A	439	20.850	14.190	73.695	1.00 40.03
ATOM	3481	O	LEU	A	439	20.214	15.064	74.255	1.00 42.22
ATOM	3482	CB	LEU	A	439	20.949	14.180	71.210	1.00 33.84
ATOM	3483	CG	LEU	A	439	21.552	14.939	70.039	1.00 32.80
ATOM	3484	CD1	LEU	A	439	20.813	14.538	68.775	1.00 34.08
ATOM	3485	CD2	LEU	A	439	21.435	16.434	70.258	1.00 23.80
ATOM	3486	N	ASN	A	440	20.810	12.953	74.076	1.00 34.03
ATOM	3487	CA	ASN	A	440	19.971	12.603	75.187	1.00 34.00
ATOM	3488	C	ASN	A	440	20.494	13.093	76.532	1.00 40.95
ATOM	3489	O	ASN	A	440	19.816	12.995	77.544	1.00 42.09

ATOM	3490	CB	ASN	A	440	19.681	11.095	75.178	1.00 24.89
ATOM	3491	CG	ASN	A	440	18.790	10.635	74.028	1.00 46.52
ATOM	3492	OD1	ASN	A	440	19.005	9.537	73.480	1.00 58.82
ATOM	3493	ND2	ASN	A	440	17.769	11.440	73.680	1.00 31.11
ATOM	3494	N	GLN	A	441	21.707	13.623	76.531	1.00 36.98
ATOM	3495	CA	GLN	A	441	22.339	14.095	77.744	1.00 35.47
ATOM	3496	C	GLN	A	441	21.879	15.478	78.067	1.00 36.00
ATOM	3497	O	GLN	A	441	22.137	16.029	79.142	1.00 34.96
ATOM	3498	CB	GLN	A	441	23.878	14.109	77.581	1.00 38.10
ATOM	3499	CG	GLN	A	441	24.504	12.692	77.422	1.00 52.06
ATOM	3500	CD	GLN	A	441	25.954	12.730	76.955	1.00 81.69
ATOM	3501	OE1	GLN	A	441	26.476	13.796	76.609	1.00 74.46
ATOM	3502	NE2	GLN	A	441	26.616	11.574	76.972	1.00 91.09
ATOM	3503	N	VAL	A	442	21.197	16.067	77.112	1.00 31.86
ATOM	3504	CA	VAL	A	442	20.753	17.411	77.384	1.00 32.78
ATOM	3505	C	VAL	A	442	19.354	17.468	77.970	1.00 38.24
ATOM	3506	O	VAL	A	442	18.468	16.700	77.588	1.00 42.83
ATOM	3507	CB	VAL	A	442	20.845	18.277	76.159	1.00 34.84
ATOM	3508	CG1	VAL	A	442	21.430	17.435	75.020	1.00 34.65
ATOM	3509	CG2	VAL	A	442	19.441	18.705	75.811	1.00 33.21
ATOM	3510	N	ASP	A	443	19.172	18.388	78.908	1.00 25.60
ATOM	3511	CA	ASP	A	443	17.931	18.634	79.616	1.00 24.57
ATOM	3512	C	ASP	A	443	16.996	19.533	78.791	1.00 32.14
ATOM	3513	O	ASP	A	443	16.744	20.732	79.073	1.00 34.77
ATOM	3514	CB	ASP	A	443	18.332	19.272	80.957	1.00 27.11
ATOM	3515	CG	ASP	A	443	17.216	19.413	81.901	1.00 39.99
ATOM	3516	OD1	ASP	A	443	16.063	19.234	81.573	1.00 44.78
ATOM	3517	OD2	ASP	A	443	17.631	19.753	83.094	1.00 56.66
ATOM	3518	N	TRP	A	444	16.525	18.914	77.722	1.00 28.30
ATOM	3519	CA	TRP	A	444	15.614	19.507	76.757	1.00 26.27
ATOM	3520	C	TRP	A	444	14.460	20.296	77.416	1.00 31.52
ATOM	3521	O	TRP	A	444	14.102	21.409	76.988	1.00 34.63
ATOM	3522	CB	TRP	A	444	15.067	18.398	75.799	1.00 21.47
ATOM	3523	CG	TRP	A	444	16.095	17.951	74.806	1.00 22.03
ATOM	3524	CD1	TRP	A	444	16.675	16.718	74.736	1.00 25.16
ATOM	3525	CD2	TRP	A	444	16.733	18.738	73.776	1.00 20.36
ATOM	3526	NE1	TRP	A	444	17.623	16.677	73.738	1.00 23.97
ATOM	3527	CE2	TRP	A	444	17.688	17.906	73.138	1.00 24.71
ATOM	3528	CE3	TRP	A	444	16.596	20.045	73.342	1.00 20.86
ATOM	3529	CZ2	TRP	A	444	18.448	18.345	72.060	1.00 24.51
ATOM	3530	CZ3	TRP	A	444	17.353	20.471	72.264	1.00 22.88
ATOM	3531	CH2	TRP	A	444	18.281	19.643	71.643	1.00 23.48
ATOM	3532	N	ASN	A	445	13.855	19.711	78.457	1.00 24.92
ATOM	3533	CA	ASN	A	445	12.723	20.326	79.113	1.00 26.30
ATOM	3534	C	ASN	A	445	13.040	21.677	79.729	1.00 30.17
ATOM	3535	O	ASN	A	445	12.291	22.660	79.547	1.00 31.86
ATOM	3536	CB	ASN	A	445	11.987	19.382	80.094	1.00 40.83
ATOM	3537	CG	ASN	A	445	10.946	20.033	81.020	1.00 87.07
ATOM	3538	OD1	ASN	A	445	11.271	20.635	82.065	1.00 86.38
ATOM	3539	ND2	ASN	A	445	9.670	19.848	80.688	1.00 71.65
ATOM	3540	N	ALA	A	446	14.147	21.687	80.436	1.00 22.70
ATOM	3541	CA	ALA	A	446	14.583	22.886	81.073	1.00 24.45
ATOM	3542	C	ALA	A	446	14.886	23.896	79.990	1.00 30.52
ATOM	3543	O	ALA	A	446	14.324	25.001	79.936	1.00 33.92
ATOM	3544	CB	ALA	A	446	15.814	22.543	81.900	1.00 25.68
ATOM	3545	N	TRP	A	447	15.776	23.494	79.102	1.00 25.24
ATOM	3546	CA	TRP	A	447	16.162	24.384	78.034	1.00 26.83
ATOM	3547	C	TRP	A	447	14.989	24.912	77.223	1.00 31.32
ATOM	3548	O	TRP	A	447	14.971	26.089	76.875	1.00 30.48
ATOM	3549	CB	TRP	A	447	17.166	23.725	77.062	1.00 25.78
ATOM	3550	CG	TRP	A	447	18.625	23.815	77.421	1.00 26.60
ATOM	3551	CD1	TRP	A	447	19.343	22.840	78.046	1.00 28.89
ATOM	3552	CD2	TRP	A	447	19.554	24.896	77.165	1.00 26.16
ATOM	3553	NE1	TRP	A	447	20.654	23.217	78.197	1.00 27.23

ATOM	3554	CE2	TRP	A	447	20.822	24.476	77.660	1.00 29.00
ATOM	3555	CE3	TRP	A	447	19.435	26.162	76.607	1.00 27.56
ATOM	3556	CZ2	TRP	A	447	21.954	25.290	77.583	1.00 27.95
ATOM	3557	CZ3	TRP	A	447	20.554	26.966	76.538	1.00 29.93
ATOM	3558	CH2	TRP	A	447	21.792	26.539	77.035	1.00 30.16
ATOM	3559	N	LEU	A	448	14.029	24.034	76.893	1.00 26.54
ATOM	3560	CA	LEU	A	448	12.896	24.421	76.052	1.00 26.92
ATOM	3561	C	LEU	A	448	11.734	25.064	76.779	1.00 36.15
ATOM	3562	O	LEU	A	448	11.089	26.031	76.304	1.00 31.19
ATOM	3563	CB	LEU	A	448	12.338	23.197	75.307	1.00 25.26
ATOM	3564	CG	LEU	A	448	13.311	22.545	74.332	1.00 28.29
ATOM	3565	CD1	LEU	A	448	12.597	21.455	73.530	1.00 30.49
ATOM	3566	CD2	LEU	A	448	13.879	23.576	73.375	1.00 21.94
ATOM	3567	N	TYR	A	449	11.472	24.455	77.924	1.00 33.14
ATOM	3568	CA	TYR	A	449	10.373	24.835	78.747	1.00 30.64
ATOM	3569	C	TYR	A	449	10.646	25.525	80.041	1.00 34.31
ATOM	3570	O	TYR	A	449	9.750	26.191	80.529	1.00 41.98
ATOM	3571	CB	TYR	A	449	9.400	23.674	78.916	1.00 29.14
ATOM	3572	CG	TYR	A	449	9.212	23.089	77.556	1.00 26.50
ATOM	3573	CD1	TYR	A	449	8.762	23.869	76.485	1.00 24.36
ATOM	3574	CD2	TYR	A	449	9.560	21.762	77.325	1.00 28.48
ATOM	3575	CE1	TYR	A	449	8.626	23.331	75.202	1.00 17.56
ATOM	3576	CE2	TYR	A	449	9.427	21.205	76.054	1.00 29.93
ATOM	3577	CZ	TYR	A	449	8.959	21.988	74.998	1.00 33.65
ATOM	3578	OH	TYR	A	449	8.840	21.415	73.762	1.00 39.47
ATOM	3579	N	SER	A	450	11.806	25.413	80.644	1.00 22.72
ATOM	3580	CA	SER	A	450	11.902	26.149	81.900	1.00 21.21
ATOM	3581	C	SER	A	450	12.278	27.625	81.749	1.00 23.98
ATOM	3582	O	SER	A	450	12.966	28.035	80.810	1.00 27.17
ATOM	3583	CB	SER	A	450	12.666	25.436	83.010	1.00 24.83
ATOM	3584	OG	SER	A	450	12.540	24.046	82.871	1.00 36.29
ATOM	3585	N	PRO	A	451	11.806	28.430	82.689	1.00 19.76
ATOM	3586	CA	PRO	A	451	12.111	29.840	82.669	1.00 18.20
ATOM	3587	C	PRO	A	451	13.461	29.988	83.271	1.00 21.72
ATOM	3588	O	PRO	A	451	14.022	29.015	83.742	1.00 24.34
ATOM	3589	CB	PRO	A	451	11.185	30.485	83.695	1.00 18.85
ATOM	3590	CG	PRO	A	451	10.836	29.390	84.677	1.00 23.13
ATOM	3591	CD	PRO	A	451	11.002	28.078	83.900	1.00 19.61
ATOM	3592	N	GLY	A	452	13.959	31.212	83.307	1.00 18.97
ATOM	3593	CA	GLY	A	452	15.241	31.444	83.922	1.00 19.09
ATOM	3594	C	GLY	A	452	16.382	31.107	83.016	1.00 26.20
ATOM	3595	O	GLY	A	452	16.191	30.916	81.819	1.00 27.37
ATOM	3596	N	LEU	A	453	17.557	31.057	83.650	1.00 25.48
ATOM	3597	CA	LEU	A	453	18.843	30.750	83.029	1.00 25.32
ATOM	3598	C	LEU	A	453	18.906	29.322	82.629	1.00 26.21
ATOM	3599	O	LEU	A	453	18.400	28.458	83.322	1.00 25.04
ATOM	3600	CB	LEU	A	453	20.042	31.119	83.938	1.00 25.46
ATOM	3601	CG	LEU	A	453	20.280	32.632	83.904	1.00 31.82
ATOM	3602	CD1	LEU	A	453	21.019	33.087	85.119	1.00 31.78
ATOM	3603	CD2	LEU	A	453	21.046	33.056	82.651	1.00 41.50
ATOM	3604	N	PRO	A	454	19.510	29.082	81.489	1.00 22.97
ATOM	3605	CA	PRO	A	454	19.585	27.747	81.003	1.00 21.60
ATOM	3606	C	PRO	A	454	20.145	26.890	82.075	1.00 26.94
ATOM	3607	O	PRO	A	454	20.923	27.359	82.893	1.00 29.09
ATOM	3608	CB	PRO	A	454	20.489	27.780	79.768	1.00 22.34
ATOM	3609	CG	PRO	A	454	20.777	29.232	79.470	1.00 23.69
ATOM	3610	CD	PRO	A	454	20.136	30.054	80.556	1.00 20.82
ATOM	3611	N	PRO	A	455	19.721	25.648	82.067	1.00 25.61
ATOM	3612	CA	PRO	A	455	20.167	24.683	83.031	1.00 24.27
ATOM	3613	C	PRO	A	455	21.661	24.568	82.991	1.00 30.95
ATOM	3614	O	PRO	A	455	22.225	24.062	83.920	1.00 33.47
ATOM	3615	CB	PRO	A	455	19.631	23.320	82.592	1.00 25.04
ATOM	3616	CG	PRO	A	455	19.149	23.497	81.162	1.00 33.02
ATOM	3617	CD	PRO	A	455	19.111	25.005	80.888	1.00 28.49

ATOM	3618	N	ILE	A	456	22.305	25.002	81.911	1.00 27.91
ATOM	3619	CA	ILE	A	456	23.764	24.893	81.821	1.00 27.82
ATOM	3620	C	ILE	A	456	24.395	26.057	81.077	1.00 34.73
ATOM	3621	O	ILE	A	456	23.737	26.769	80.293	1.00 37.01
ATOM	3622	CB	ILE	A	456	24.228	23.540	81.259	1.00 31.34
ATOM	3623	CG1	ILE	A	456	25.721	23.305	81.417	1.00 29.78
ATOM	3624	CG2	ILE	A	456	23.865	23.369	79.788	1.00 32.96
ATOM	3625	CD1	ILE	A	456	26.054	21.852	81.116	1.00 23.94
ATOM	3626	N	LYS	A	457	25.680	26.252	81.334	1.00 30.52
ATOM	3627	CA	LYS	A	457	26.405	27.335	80.707	1.00 30.21
ATOM	3628	C	LYS	A	457	27.515	26.808	79.835	1.00 32.14
ATOM	3629	O	LYS	A	457	28.328	26.037	80.273	1.00 33.07
ATOM	3630	CB	LYS	A	457	26.953	28.264	81.749	1.00 32.38
ATOM	3631	CG	LYS	A	457	27.818	29.327	81.121	1.00 34.64
ATOM	3632	CD	LYS	A	457	28.288	30.306	82.166	1.00 13.41
ATOM	3633	CE	LYS	A	457	28.803	31.596	81.565	1.00 18.04
ATOM	3634	NZ	LYS	A	457	28.974	32.643	82.595	1.00 26.77
ATOM	3635	N	PRO	A	458	27.567	27.208	78.589	1.00 27.50
ATOM	3636	CA	PRO	A	458	28.630	26.675	77.737	1.00 26.85
ATOM	3637	C	PRO	A	458	29.994	27.147	78.185	1.00 26.89
ATOM	3638	O	PRO	A	458	30.128	27.876	79.167	1.00 24.86
ATOM	3639	CB	PRO	A	458	28.335	27.191	76.316	1.00 29.41
ATOM	3640	CG	PRO	A	458	26.952	27.864	76.375	1.00 33.24
ATOM	3641	CD	PRO	A	458	26.574	28.044	77.848	1.00 26.12
ATOM	3642	N	ASN	A	459	31.005	26.754	77.440	1.00 22.13
ATOM	3643	CA	ASN	A	459	32.359	27.191	77.735	1.00 22.29
ATOM	3644	C	ASN	A	459	32.751	28.325	76.820	1.00 30.27
ATOM	3645	O	ASN	A	459	32.451	28.296	75.617	1.00 32.89
ATOM	3646	CB	ASN	A	459	33.315	26.060	77.494	1.00 25.03
ATOM	3647	CG	ASN	A	459	32.766	24.846	78.155	1.00 49.54
ATOM	3648	OD1	ASN	A	459	32.618	24.822	79.383	1.00 50.09
ATOM	3649	ND2	ASN	A	459	32.411	23.870	77.332	1.00 38.39
ATOM	3650	N	TYR	A	460	33.448	29.316	77.380	1.00 25.58
ATOM	3651	CA	TYR	A	460	33.851	30.493	76.625	1.00 23.89
ATOM	3652	C	TYR	A	460	35.298	30.853	76.745	1.00 34.20
ATOM	3653	O	TYR	A	460	35.849	30.862	77.839	1.00 35.27
ATOM	3654	CB	TYR	A	460	33.120	31.708	77.171	1.00 24.38
ATOM	3655	CG	TYR	A	460	31.636	31.631	77.024	1.00 26.98
ATOM	3656	CD1	TYR	A	460	31.029	32.011	75.829	1.00 30.69
ATOM	3657	CD2	TYR	A	460	30.838	31.168	78.064	1.00 25.70
ATOM	3658	CE1	TYR	A	460	29.644	31.952	75.684	1.00 28.77
ATOM	3659	CE2	TYR	A	460	29.453	31.096	77.938	1.00 25.24
ATOM	3660	CZ	TYR	A	460	28.863	31.496	76.741	1.00 24.49
ATOM	3661	OH	TYR	A	460	27.519	31.443	76.587	1.00 28.39
ATOM	3662	N	ASP	A	461	35.893	31.227	75.616	1.00 30.58
ATOM	3663	CA	ASP	A	461	37.268	31.640	75.654	1.00 27.51
ATOM	3664	C	ASP	A	461	37.319	32.941	76.464	1.00 23.53
ATOM	3665	O	ASP	A	461	36.377	33.704	76.396	1.00 26.62
ATOM	3666	CB	ASP	A	461	37.821	31.784	74.218	1.00 27.30
ATOM	3667	CG	ASP	A	461	39.137	32.466	74.260	1.00 32.53
ATOM	3668	OD1	ASP	A	461	39.262	33.672	74.334	1.00 39.66
ATOM	3669	OD2	ASP	A	461	40.130	31.628	74.306	1.00 44.34
ATOM	3670	N	MET	A	462	38.375	33.234	77.224	1.00 17.26
ATOM	3671	CA	MET	A	462	38.396	34.511	78.008	1.00 18.66
ATOM	3672	C	MET	A	462	39.299	35.634	77.485	1.00 24.02
ATOM	3673	O	MET	A	462	39.336	36.738	78.011	1.00 24.56
ATOM	3674	CB	MET	A	462	38.818	34.186	79.431	1.00 22.99
ATOM	3675	CG	MET	A	462	37.808	33.209	80.025	1.00 28.98
ATOM	3676	SD	MET	A	462	36.166	33.969	79.951	1.00 33.22
ATOM	3677	CE	MET	A	462	36.420	35.300	81.153	1.00 27.89
ATOM	3678	N	THR	A	463	40.067	35.348	76.461	1.00 22.57
ATOM	3679	CA	THR	A	463	41.015	36.285	75.911	1.00 22.64
ATOM	3680	C	THR	A	463	40.690	37.738	75.961	1.00 33.12
ATOM	3681	O	THR	A	463	41.372	38.493	76.640	1.00 35.27

ATOM	3682	CB	THR	A	463	41.574	35.929	74.536	1.00 29.80
ATOM	3683	OG1	THR	A	463	41.939	34.576	74.509	1.00 26.74
ATOM	3684	CG2	THR	A	463	42.797	36.793	74.224	1.00 18.79
ATOM	3685	N	LEU	A	464	39.700	38.141	75.177	1.00 30.50
ATOM	3686	CA	LEU	A	464	39.293	39.533	75.061	1.00 29.15
ATOM	3687	C	LEU	A	464	38.490	40.067	76.216	1.00 34.24
ATOM	3688	O	LEU	A	464	38.439	41.270	76.422	1.00 37.12
ATOM	3689	CB	LEU	A	464	38.537	39.767	73.743	1.00 29.20
ATOM	3690	CG	LEU	A	464	39.393	39.394	72.527	1.00 33.73
ATOM	3691	CD1	LEU	A	464	38.609	39.565	71.217	1.00 32.72
ATOM	3692	CD2	LEU	A	464	40.648	40.261	72.499	1.00 26.22
ATOM	3693	N	THR	A	465	37.855	39.167	76.964	1.00 30.71
ATOM	3694	CA	THR	A	465	37.005	39.496	78.103	1.00 28.58
ATOM	3695	C	THR	A	465	37.800	39.893	79.324	1.00 30.69
ATOM	3696	O	THR	A	465	37.530	40.865	80.030	1.00 31.27
ATOM	3697	CB	THR	A	465	36.016	38.328	78.372	1.00 35.85
ATOM	3698	OG1	THR	A	465	35.101	38.212	77.296	1.00 50.93
ATOM	3699	CG2	THR	A	465	35.255	38.451	79.690	1.00 26.34
ATOM	3700	N	ASN	A	466	38.802	39.111	79.568	1.00 24.40
ATOM	3701	CA	ASN	A	466	39.635	39.375	80.688	1.00 23.11
ATOM	3702	C	ASN	A	466	39.899	40.856	80.967	1.00 28.37
ATOM	3703	O	ASN	A	466	39.763	41.270	82.120	1.00 27.03
ATOM	3704	CB	ASN	A	466	40.921	38.543	80.629	1.00 20.30
ATOM	3705	CG	ASN	A	466	40.709	37.145	81.155	1.00 32.26
ATOM	3706	OD1	ASN	A	466	41.384	36.191	80.723	1.00 29.29
ATOM	3707	ND2	ASN	A	466	39.775	37.015	82.111	1.00 28.19
ATOM	3708	N	ALA	A	467	40.306	41.666	79.967	1.00 27.97
ATOM	3709	CA	ALA	A	467	40.587	43.079	80.295	1.00 26.66
ATOM	3710	C	ALA	A	467	39.352	43.827	80.720	1.00 31.78
ATOM	3711	O	ALA	A	467	39.406	44.845	81.393	1.00 31.71
ATOM	3712	CB	ALA	A	467	41.365	43.837	79.256	1.00 25.99
ATOM	3713	N	CYS	A	468	38.217	43.277	80.336	1.00 28.06
ATOM	3714	CA	CYS	A	468	36.942	43.862	80.693	1.00 25.80
ATOM	3715	C	CYS	A	468	36.668	43.619	82.165	1.00 26.47
ATOM	3716	O	CYS	A	468	36.469	44.517	82.963	1.00 27.99
ATOM	3717	CB	CYS	A	468	35.882	43.376	79.696	1.00 24.56
ATOM	3718	SG	CYS	A	468	36.455	43.873	78.049	1.00 27.76
ATOM	3719	N	ILE	A	469	36.752	42.384	82.540	1.00 24.34
ATOM	3720	CA	ILE	A	469	36.599	42.052	83.921	1.00 25.23
ATOM	3721	C	ILE	A	469	37.560	42.800	84.876	1.00 28.13
ATOM	3722	O	ILE	A	469	37.175	43.220	85.950	1.00 29.54
ATOM	3723	CB	ILE	A	469	36.858	40.574	84.068	1.00 27.23
ATOM	3724	CG1	ILE	A	469	35.956	39.801	83.112	1.00 26.94
ATOM	3725	CG2	ILE	A	469	36.537	40.208	85.496	1.00 25.56
ATOM	3726	CD1	ILE	A	469	36.247	38.298	83.085	1.00 45.50
ATOM	3727	N	ALA	A	470	38.830	42.960	84.534	1.00 23.28
ATOM	3728	CA	ALA	A	470	39.749	43.621	85.461	1.00 22.23
ATOM	3729	C	ALA	A	470	39.392	45.038	85.808	1.00 30.29
ATOM	3730	O	ALA	A	470	39.474	45.451	86.986	1.00 32.82
ATOM	3731	CB	ALA	A	470	41.218	43.502	85.074	1.00 21.98
ATOM	3732	N	LEU	A	471	39.007	45.760	84.759	1.00 23.53
ATOM	3733	CA	LEU	A	471	38.643	47.173	84.834	1.00 18.39
ATOM	3734	C	LEU	A	471	37.333	47.373	85.569	1.00 26.57
ATOM	3735	O	LEU	A	471	37.210	48.208	86.462	1.00 30.48
ATOM	3736	CB	LEU	A	471	38.676	47.827	83.444	1.00 15.51
ATOM	3737	CG	LEU	A	471	38.671	49.325	83.539	1.00 24.20
ATOM	3738	CD1	LEU	A	471	39.754	49.795	84.513	1.00 24.86
ATOM	3739	CD2	LEU	A	471	38.876	49.941	82.156	1.00 26.35
ATOM	3740	N	SER	A	472	36.351	46.570	85.222	1.00 25.31
ATOM	3741	CA	SER	A	472	35.080	46.674	85.901	1.00 27.56
ATOM	3742	C	SER	A	472	35.260	46.477	87.396	1.00 33.46
ATOM	3743	O	SER	A	472	34.800	47.292	88.214	1.00 32.85
ATOM	3744	CB	SER	A	472	33.989	45.714	85.393	1.00 32.06
ATOM	3745	OG	SER	A	472	34.492	44.774	84.470	1.00 48.56

ATOM	3746	N	GLN	A	473	35.911	45.350	87.736	1.00 27.52
ATOM	3747	CA	GLN	A	473	36.170	44.971	89.108	1.00 24.10
ATOM	3748	C	GLN	A	473	36.866	46.096	89.836	1.00 25.18
ATOM	3749	O	GLN	A	473	36.534	46.458	90.969	1.00 21.62
ATOM	3750	CB	GLN	A	473	36.994	43.671	89.148	1.00 25.86
ATOM	3751	CG	GLN	A	473	36.128	42.402	89.118	1.00 32.72
ATOM	3752	CD	GLN	A	473	34.970	42.504	90.090	1.00 46.08
ATOM	3753	OE1	GLN	A	473	35.165	42.422	91.308	1.00 40.73
ATOM	3754	NE2	GLN	A	473	33.761	42.692	89.559	1.00 28.28
ATOM	3755	N	ARG	A	474	37.855	46.656	89.161	1.00 24.00
ATOM	3756	CA	ARG	A	474	38.562	47.765	89.779	1.00 24.46
ATOM	3757	C	ARG	A	474	37.609	48.893	90.141	1.00 29.31
ATOM	3758	O	ARG	A	474	37.620	49.447	91.242	1.00 33.13
ATOM	3759	CB	ARG	A	474	39.682	48.290	88.898	1.00 20.19
ATOM	3760	CG	ARG	A	474	40.866	47.352	88.831	1.00 28.48
ATOM	3761	CD	ARG	A	474	41.871	47.869	87.832	1.00 34.41
ATOM	3762	NE	ARG	A	474	42.258	49.245	88.093	1.00 40.09
ATOM	3763	CZ	ARG	A	474	42.927	49.938	87.185	1.00 51.25
ATOM	3764	NH1	ARG	A	474	43.220	49.376	86.019	1.00 24.79
ATOM	3765	NH2	ARG	A	474	43.316	51.199	87.444	1.00 20.43
ATOM	3766	N	TRP	A	475	36.791	49.259	89.178	1.00 25.32
ATOM	3767	CA	TRP	A	475	35.862	50.332	89.400	1.00 26.77
ATOM	3768	C	TRP	A	475	34.881	49.962	90.474	1.00 27.52
ATOM	3769	O	TRP	A	475	34.749	50.633	91.475	1.00 29.64
ATOM	3770	CB	TRP	A	475	35.199	50.804	88.093	1.00 27.95
ATOM	3771	CG	TRP	A	475	36.047	51.819	87.361	1.00 32.11
ATOM	3772	CD1	TRP	A	475	36.873	51.592	86.298	1.00 35.65
ATOM	3773	CD2	TRP	A	475	36.161	53.217	87.648	1.00 31.62
ATOM	3774	NE1	TRP	A	475	37.484	52.748	85.904	1.00 34.92
ATOM	3775	CE2	TRP	A	475	37.054	53.763	86.707	1.00 36.16
ATOM	3776	CE3	TRP	A	475	35.588	54.040	88.606	1.00 32.63
ATOM	3777	CZ2	TRP	A	475	37.372	55.112	86.719	1.00 36.24
ATOM	3778	CZ3	TRP	A	475	35.897	55.375	88.616	1.00 34.74
ATOM	3779	CH2	TRP	A	475	36.777	55.901	87.685	1.00 35.77
ATOM	3780	N	ILE	A	476	34.234	48.847	90.279	1.00 26.36
ATOM	3781	CA	ILE	A	476	33.268	48.386	91.235	1.00 28.33
ATOM	3782	C	ILE	A	476	33.771	48.315	92.681	1.00 34.20
ATOM	3783	O	ILE	A	476	33.056	48.595	93.637	1.00 36.89
ATOM	3784	CB	ILE	A	476	32.722	47.070	90.761	1.00 32.23
ATOM	3785	CG1	ILE	A	476	31.993	47.308	89.443	1.00 30.49
ATOM	3786	CG2	ILE	A	476	31.864	46.376	91.851	1.00 34.86
ATOM	3787	CD1	ILE	A	476	31.595	46.005	88.756	1.00 33.04
ATOM	3788	N	THR	A	477	35.010	47.934	92.860	1.00 27.27
ATOM	3789	CA	THR	A	477	35.558	47.846	94.194	1.00 24.15
ATOM	3790	C	THR	A	477	36.416	49.052	94.523	1.00 27.30
ATOM	3791	O	THR	A	477	37.120	49.065	95.519	1.00 27.36
ATOM	3792	CB	THR	A	477	36.402	46.578	94.257	1.00 32.13
ATOM	3793	OG1	THR	A	477	37.593	46.848	93.557	1.00 29.48
ATOM	3794	CG2	THR	A	477	35.634	45.470	93.530	1.00 16.94
ATOM	3795	N	ALA	A	478	36.371	50.097	93.695	1.00 22.33
ATOM	3796	CA	ALA	A	478	37.164	51.260	93.988	1.00 20.44
ATOM	3797	C	ALA	A	478	36.890	51.843	95.390	1.00 32.94
ATOM	3798	O	ALA	A	478	35.786	51.756	95.922	1.00 34.38
ATOM	3799	CB	ALA	A	478	36.938	52.343	92.942	1.00 19.26
ATOM	3800	N	LYS	A	479	37.931	52.469	95.970	1.00 29.65
ATOM	3801	CA	LYS	A	479	37.899	53.168	97.243	1.00 27.30
ATOM	3802	C	LYS	A	479	38.575	54.512	97.051	1.00 36.54
ATOM	3803	O	LYS	A	479	39.378	54.692	96.118	1.00 34.13
ATOM	3804	CB	LYS	A	479	38.457	52.410	98.417	1.00 28.01
ATOM	3805	CG	LYS	A	479	37.696	51.116	98.631	1.00 51.38
ATOM	3806	CD	LYS	A	479	37.115	50.880	100.021	1.00 67.24
ATOM	3807	CE	LYS	A	479	35.804	50.103	99.931	1.00 87.12
ATOM	3808	NZ	LYS	A	479	35.711	48.948	100.841	1.00 85.55
ATOM	3809	N	GLU	A	480	38.241	55.477	97.900	1.00 36.30

ATOM	3810	CA	GLU	A	480	38.843	56.793	97.751	1.00 34.79
ATOM	3811	C	GLU	A	480	40.261	56.707	97.220	1.00 34.79
ATOM	3812	O	GLU	A	480	40.613	57.332	96.234	1.00 34.10
ATOM	3813	CB	GLU	A	480	38.899	57.565	99.078	1.00 36.21
ATOM	3814	CG	GLU	A	480	37.709	58.500	99.303	1.00 63.85
ATOM	3815	CD	GLU	A	480	37.601	59.511	98.214	1.00100.00
ATOM	3816	OE1	GLU	A	480	38.457	59.648	97.357	1.00100.00
ATOM	3817	OE2	GLU	A	480	36.491	60.209	98.288	1.00100.00
ATOM	3818	N	ASP	A	481	41.080	55.946	97.904	1.00 24.69
ATOM	3819	CA	ASP	A	481	42.451	55.860	97.519	1.00 23.87
ATOM	3820	C	ASP	A	481	42.771	55.314	96.132	1.00 34.51
ATOM	3821	O	ASP	A	481	43.925	55.312	95.721	1.00 39.44
ATOM	3822	CB	ASP	A	481	43.262	55.155	98.611	1.00 25.29
ATOM	3823	CG	ASP	A	481	43.072	53.668	98.575	1.00 39.58
ATOM	3824	OD1	ASP	A	481	42.471	53.029	97.708	1.00 46.00
ATOM	3825	OD2	ASP	A	481	43.698	53.107	99.567	1.00 39.59
ATOM	3826	N	ASP	A	482	41.788	54.881	95.373	1.00 30.70
ATOM	3827	CA	ASP	A	482	42.098	54.379	94.024	1.00 31.73
ATOM	3828	C	ASP	A	482	41.725	55.307	92.859	1.00 34.17
ATOM	3829	O	ASP	A	482	42.158	55.150	91.717	1.00 35.45
ATOM	3830	CB	ASP	A	482	41.399	53.022	93.756	1.00 33.31
ATOM	3831	CG	ASP	A	482	41.686	51.970	94.779	1.00 38.90
ATOM	3832	OD1	ASP	A	482	42.810	51.514	94.992	1.00 42.45
ATOM	3833	OD2	ASP	A	482	40.606	51.625	95.440	1.00 40.17
ATOM	3834	N	LEU	A	483	40.863	56.246	93.146	1.00 29.93
ATOM	3835	CA	LEU	A	483	40.352	57.159	92.160	1.00 27.80
ATOM	3836	C	LEU	A	483	41.434	57.943	91.410	1.00 40.70
ATOM	3837	O	LEU	A	483	41.386	58.102	90.180	1.00 40.76
ATOM	3838	CB	LEU	A	483	39.265	58.049	92.819	1.00 22.54
ATOM	3839	CG	LEU	A	483	38.148	57.240	93.488	1.00 20.75
ATOM	3840	CD1	LEU	A	483	37.170	58.165	94.197	1.00 19.29
ATOM	3841	CD2	LEU	A	483	37.389	56.467	92.414	1.00 21.46
ATOM	3842	N	ASN	A	484	42.410	58.446	92.162	1.00 36.15
ATOM	3843	CA	ASN	A	484	43.459	59.225	91.571	1.00 34.08
ATOM	3844	C	ASN	A	484	44.168	58.524	90.429	1.00 39.51
ATOM	3845	O	ASN	A	484	44.456	59.091	89.359	1.00 38.59
ATOM	3846	CB	ASN	A	484	44.495	59.602	92.618	1.00 34.26
ATOM	3847	CG	ASN	A	484	45.807	59.955	91.941	1.00100.00
ATOM	3848	OD1	ASN	A	484	45.878	60.940	91.171	1.00100.00
ATOM	3849	ND2	ASN	A	484	46.836	59.134	92.186	1.00100.00
ATOM	3850	N	SER	A	485	44.472	57.268	90.698	1.00 35.37
ATOM	3851	CA	SER	A	485	45.202	56.417	89.791	1.00 32.79
ATOM	3852	C	SER	A	485	44.522	56.140	88.484	1.00 32.26
ATOM	3853	O	SER	A	485	45.159	55.925	87.463	1.00 32.44
ATOM	3854	CB	SER	A	485	45.565	55.132	90.477	1.00 38.65
ATOM	3855	OG	SER	A	485	46.040	55.437	91.777	1.00 62.66
ATOM	3856	N	PHE	A	486	43.222	56.110	88.491	1.00 27.13
ATOM	3857	CA	PHE	A	486	42.631	55.809	87.233	1.00 28.26
ATOM	3858	C	PHE	A	486	43.193	56.772	86.264	1.00 32.12
ATOM	3859	O	PHE	A	486	43.423	57.910	86.604	1.00 32.02
ATOM	3860	CB	PHE	A	486	41.101	55.819	87.198	1.00 31.01
ATOM	3861	CG	PHE	A	486	40.471	54.807	88.132	1.00 27.04
ATOM	3862	CD1	PHE	A	486	40.504	53.425	87.911	1.00 22.43
ATOM	3863	CD2	PHE	A	486	39.805	55.293	89.253	1.00 21.40
ATOM	3864	CE1	PHE	A	486	39.896	52.538	88.804	1.00 19.69
ATOM	3865	CE2	PHE	A	486	39.224	54.426	90.174	1.00 19.20
ATOM	3866	CZ	PHE	A	486	39.245	53.051	89.927	1.00 15.13
ATOM	3867	N	ASN	A	487	43.455	56.279	85.089	1.00 34.97
ATOM	3868	CA	ASN	A	487	44.032	57.092	84.070	1.00 38.06
ATOM	3869	C	ASN	A	487	43.491	56.622	82.758	1.00 43.55
ATOM	3870	O	ASN	A	487	42.951	55.537	82.604	1.00 46.30
ATOM	3871	CB	ASN	A	487	45.591	57.038	84.085	1.00 43.93
ATOM	3872	CG	ASN	A	487	46.196	58.169	83.302	1.00 56.10
ATOM	3873	OD1	ASN	A	487	46.057	58.189	82.077	1.00 42.12

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ATOM   3874  ND2 ASN A 487      46.829  59.112  84.007  1.00 65.62
ATOM   3875  N   ALA A 488      43.662  57.435  81.781  1.00 39.34
ATOM   3876  CA  ALA A 488      43.201  57.055  80.472  1.00 38.25
ATOM   3877  C   ALA A 488      44.024  55.900  79.809  1.00 43.58
ATOM   3878  O   ALA A 488      43.596  55.317  78.834  1.00 44.11
ATOM   3879  CB  ALA A 488      43.153  58.314  79.621  1.00 37.54
ATOM   3880  N   THR A 489      45.207  55.555  80.314  1.00 38.34
ATOM   3881  CA  THR A 489      45.996  54.499  79.715  1.00 36.16
ATOM   3882  C   THR A 489      45.270  53.181  79.792  1.00 45.74
ATOM   3883  O   THR A 489      45.476  52.233  79.057  1.00 47.78
ATOM   3884  CB  THR A 489      47.296  54.458  80.503  1.00 31.01
ATOM   3885  OG1 THR A 489      46.961  54.457  81.872  1.00 35.33
ATOM   3886  CG2 THR A 489      47.993  55.771  80.229  1.00 28.28
ATOM   3887  N   ASP A 490      44.337  53.182  80.708  1.00 46.75
ATOM   3888  CA  ASP A 490      43.560  52.018  80.972  1.00 51.49
ATOM   3889  C   ASP A 490      42.759  51.515  79.786  1.00 52.21
ATOM   3890  O   ASP A 490      42.396  50.342  79.651  1.00 54.75
ATOM   3891  CB  ASP A 490      42.676  52.345  82.184  1.00 54.04
ATOM   3892  CG  ASP A 490      43.413  52.884  83.380  1.00 53.83
ATOM   3893  OD1 ASP A 490      44.621  52.777  83.616  1.00 62.93
ATOM   3894  OD2 ASP A 490      42.565  53.446  84.165  1.00 35.66
ATOM   3895  N   LEU A 491      42.486  52.450  78.938  1.00 42.42
ATOM   3896  CA  LEU A 491      41.752  52.250  77.723  1.00 43.54
ATOM   3897  C   LEU A 491      42.712  51.977  76.585  1.00 43.97
ATOM   3898  O   LEU A 491      42.340  51.438  75.588  1.00 42.53
ATOM   3899  CB  LEU A 491      40.984  53.528  77.421  1.00 44.89
ATOM   3900  CG  LEU A 491      39.794  53.747  78.338  1.00 48.31
ATOM   3901  CD1 LEU A 491      38.558  54.171  77.552  1.00 49.16
ATOM   3902  CD2 LEU A 491      39.377  52.494  79.125  1.00 39.24
ATOM   3903  N   LYS A 492      43.958  52.403  76.754  1.00 42.32
ATOM   3904  CA  LYS A 492      44.999  52.320  75.696  1.00 44.57
ATOM   3905  C   LYS A 492      44.826  51.165  74.680  1.00 49.08
ATOM   3906  O   LYS A 492      44.810  51.343  73.473  1.00 49.66
ATOM   3907  CB  LYS A 492      46.359  52.177  76.401  1.00 48.47
ATOM   3908  CG  LYS A 492      47.487  52.883  75.629  1.00 88.73
ATOM   3909  CD  LYS A 492      48.852  52.537  76.197  1.00100.00
ATOM   3910  CE  LYS A 492      48.786  51.460  77.300  1.00100.00
ATOM   3911  NZ  LYS A 492      50.103  50.896  77.541  1.00100.00
ATOM   3912  N   ASP A 493      44.711  49.917  75.227  1.00 41.86
ATOM   3913  CA  ASP A 493      44.664  48.740  74.372  1.00 40.17
ATOM   3914  C   ASP A 493      43.220  48.162  74.215  1.00 44.29
ATOM   3915  O   ASP A 493      43.031  46.973  73.889  1.00 42.00
ATOM   3916  CB  ASP A 493      45.560  47.699  75.015  1.00 41.52
ATOM   3917  CG  ASP A 493      47.021  48.130  74.956  1.00 67.01
ATOM   3918  OD1 ASP A 493      47.467  48.451  73.856  1.00 77.10
ATOM   3919  OD2 ASP A 493      47.678  48.131  75.984  1.00 57.19
ATOM   3920  N   LEU A 494      42.193  49.005  74.475  1.00 40.69
ATOM   3921  CA  LEU A 494      40.789  48.512  74.526  1.00 36.32
ATOM   3922  C   LEU A 494      39.992  48.877  73.245  1.00 37.76
ATOM   3923  O   LEU A 494      39.897  50.029  72.863  1.00 38.93
ATOM   3924  CB  LEU A 494      40.098  49.125  75.733  1.00 32.52
ATOM   3925  CG  LEU A 494      40.376  48.433  77.063  1.00 30.66
ATOM   3926  CD1 LEU A 494      39.229  48.580  78.052  1.00 30.39
ATOM   3927  CD2 LEU A 494      40.611  46.925  76.918  1.00 23.54
ATOM   3928  N   SER A 495      39.477  47.825  72.631  1.00 25.56
ATOM   3929  CA  SER A 495      38.674  48.017  71.457  1.00 22.23
ATOM   3930  C   SER A 495      37.344  48.670  71.856  1.00 31.27
ATOM   3931  O   SER A 495      36.968  48.706  73.038  1.00 31.21
ATOM   3932  CB  SER A 495      38.380  46.705  70.795  1.00 20.88
ATOM   3933  OG  SER A 495      37.192  46.143  71.317  1.00 33.60
ATOM   3934  N   SER A 496      36.627  49.184  70.865  1.00 29.48
ATOM   3935  CA  SER A 496      35.363  49.821  71.139  1.00 26.67
ATOM   3936  C   SER A 496      34.495  48.747  71.744  1.00 29.54
ATOM   3937  O   SER A 496      33.744  48.960  72.697  1.00 24.80
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ATOM	3938	CB	SER	A	496	34.760	50.441	69.894	1.00 24.67
ATOM	3939	OG	SER	A	496	33.749	49.597	69.397	1.00 48.80
ATOM	3940	N	HIS	A	497	34.674	47.547	71.219	1.00 26.61
ATOM	3941	CA	HIS	A	497	33.949	46.383	71.750	1.00 29.22
ATOM	3942	C	HIS	A	497	34.156	46.148	73.275	1.00 37.24
ATOM	3943	O	HIS	A	497	33.238	45.863	74.041	1.00 38.21
ATOM	3944	CB	HIS	A	497	34.364	45.106	70.978	1.00 30.69
ATOM	3945	CG	HIS	A	497	34.182	45.348	69.545	1.00 34.29
ATOM	3946	ND1	HIS	A	497	32.943	45.204	68.962	1.00 35.42
ATOM	3947	CD2	HIS	A	497	35.054	45.833	68.622	1.00 36.68
ATOM	3948	CE1	HIS	A	497	33.075	45.531	67.702	1.00 35.05
ATOM	3949	NE2	HIS	A	497	34.330	45.932	67.462	1.00 35.88
ATOM	3950	N	GLN	A	498	35.406	46.243	73.715	1.00 33.56
ATOM	3951	CA	GLN	A	498	35.737	46.008	75.094	1.00 29.69
ATOM	3952	C	GLN	A	498	35.263	47.122	75.965	1.00 27.11
ATOM	3953	O	GLN	A	498	34.842	46.930	77.089	1.00 23.92
ATOM	3954	CB	GLN	A	498	37.221	45.659	75.248	1.00 29.95
ATOM	3955	CG	GLN	A	498	37.582	44.317	74.544	1.00 25.78
ATOM	3956	CD	GLN	A	498	39.074	44.084	74.535	1.00 28.64
ATOM	3957	OE1	GLN	A	498	39.796	44.891	73.960	1.00 26.62
ATOM	3958	NE2	GLN	A	498	39.561	43.049	75.218	1.00 20.96
ATOM	3959	N	LEU	A	499	35.289	48.301	75.431	1.00 27.13
ATOM	3960	CA	LEU	A	499	34.819	49.396	76.229	1.00 29.32
ATOM	3961	C	LEU	A	499	33.351	49.162	76.632	1.00 28.39
ATOM	3962	O	LEU	A	499	32.893	49.361	77.780	1.00 29.41
ATOM	3963	CB	LEU	A	499	34.991	50.709	75.436	1.00 31.70
ATOM	3964	CG	LEU	A	499	36.242	51.512	75.788	1.00 39.76
ATOM	3965	CD1	LEU	A	499	37.335	50.572	76.278	1.00 42.91
ATOM	3966	CD2	LEU	A	499	36.718	52.268	74.555	1.00 39.08
ATOM	3967	N	ASN	A	500	32.606	48.737	75.642	1.00 15.23
ATOM	3968	CA	ASN	A	500	31.213	48.508	75.828	1.00 13.44
ATOM	3969	C	ASN	A	500	30.919	47.455	76.864	1.00 18.98
ATOM	3970	O	ASN	A	500	29.997	47.602	77.705	1.00 19.01
ATOM	3971	CB	ASN	A	500	30.604	48.129	74.476	1.00 12.21
ATOM	3972	CG	ASN	A	500	29.093	48.214	74.426	1.00 37.49
ATOM	3973	OD1	ASN	A	500	28.433	49.151	74.930	1.00 36.17
ATOM	3974	ND2	ASN	A	500	28.542	47.218	73.787	1.00 18.34
ATOM	3975	N	GLU	A	501	31.699	46.366	76.743	1.00 14.20
ATOM	3976	CA	GLU	A	501	31.626	45.224	77.625	1.00 13.27
ATOM	3977	C	GLU	A	501	31.948	45.676	79.063	1.00 21.59
ATOM	3978	O	GLU	A	501	31.175	45.463	80.009	1.00 25.02
ATOM	3979	CB	GLU	A	501	32.446	44.057	77.053	1.00 14.95
ATOM	3980	CG	GLU	A	501	32.371	42.827	77.989	1.00 30.40
ATOM	3981	CD	GLU	A	501	30.946	42.399	78.199	1.00 39.28
ATOM	3982	OE1	GLU	A	501	30.050	42.672	77.413	1.00 76.70
ATOM	3983	OE2	GLU	A	501	30.780	41.694	79.292	1.00 46.10
ATOM	3984	N	PHE	A	502	33.059	46.400	79.226	1.00 18.07
ATOM	3985	CA	PHE	A	502	33.395	46.952	80.530	1.00 21.54
ATOM	3986	C	PHE	A	502	32.179	47.679	81.125	1.00 23.38
ATOM	3987	O	PHE	A	502	31.786	47.491	82.301	1.00 21.47
ATOM	3988	CB	PHE	A	502	34.507	48.012	80.327	1.00 26.05
ATOM	3989	CG	PHE	A	502	34.590	49.082	81.393	1.00 30.41
ATOM	3990	CD1	PHE	A	502	35.085	48.781	82.662	1.00 29.68
ATOM	3991	CD2	PHE	A	502	34.211	50.402	81.132	1.00 39.16
ATOM	3992	CE1	PHE	A	502	35.183	49.773	83.638	1.00 31.12
ATOM	3993	CE2	PHE	A	502	34.305	51.414	82.096	1.00 40.46
ATOM	3994	CZ	PHE	A	502	34.812	51.090	83.352	1.00 35.41
ATOM	3995	N	LEU	A	503	31.613	48.557	80.288	1.00 18.39
ATOM	3996	CA	LEU	A	503	30.487	49.343	80.692	1.00 22.78
ATOM	3997	C	LEU	A	503	29.337	48.491	81.178	1.00 31.04
ATOM	3998	O	LEU	A	503	28.768	48.784	82.243	1.00 29.23
ATOM	3999	CB	LEU	A	503	30.002	50.325	79.619	1.00 24.68
ATOM	4000	CG	LEU	A	503	30.888	51.571	79.465	1.00 27.47
ATOM	4001	CD1	LEU	A	503	30.415	52.376	78.259	1.00 24.86

ATOM	4002	CD2	LEU	A	503	30.860	52.420	80.733	1.00 20.54
ATOM	4003	N	ALA	A	504	29.012	47.444	80.378	1.00 27.79
ATOM	4004	CA	ALA	A	504	27.911	46.474	80.643	1.00 24.63
ATOM	4005	C	ALA	A	504	28.140	45.752	81.939	1.00 27.71
ATOM	4006	O	ALA	A	504	27.265	45.577	82.817	1.00 28.62
ATOM	4007	CB	ALA	A	504	27.762	45.482	79.496	1.00 23.87
ATOM	4008	N	GLN	A	505	29.382	45.344	82.066	1.00 22.16
ATOM	4009	CA	GLN	A	505	29.738	44.710	83.299	1.00 21.02
ATOM	4010	C	GLN	A	505	29.489	45.737	84.423	1.00 31.26
ATOM	4011	O	GLN	A	505	28.787	45.507	85.413	1.00 32.31
ATOM	4012	CB	GLN	A	505	31.202	44.209	83.270	1.00 18.95
ATOM	4013	CG	GLN	A	505	31.367	42.881	82.495	1.00 13.72
ATOM	4014	CD	GLN	A	505	32.806	42.549	82.136	1.00 31.75
ATOM	4015	OE1	GLN	A	505	33.796	42.969	82.768	1.00 43.14
ATOM	4016	NE2	GLN	A	505	32.923	41.781	81.085	1.00 39.34
ATOM	4017	N	THR	A	506	30.056	46.918	84.263	1.00 25.95
ATOM	4018	CA	THR	A	506	29.855	47.864	85.302	1.00 23.64
ATOM	4019	C	THR	A	506	28.411	48.101	85.579	1.00 23.89
ATOM	4020	O	THR	A	506	27.923	47.999	86.696	1.00 22.75
ATOM	4021	CB	THR	A	506	30.600	49.130	85.008	1.00 23.72
ATOM	4022	OG1	THR	A	506	31.938	48.749	84.742	1.00 27.18
ATOM	4023	CG2	THR	A	506	30.502	49.961	86.260	1.00 11.12
ATOM	4024	N	LEU	A	507	27.727	48.408	84.518	1.00 17.92
ATOM	4025	CA	LEU	A	507	26.334	48.683	84.604	1.00 17.22
ATOM	4026	C	LEU	A	507	25.618	47.683	85.442	1.00 25.65
ATOM	4027	O	LEU	A	507	24.816	48.073	86.266	1.00 27.85
ATOM	4028	CB	LEU	A	507	25.693	48.686	83.224	1.00 17.85
ATOM	4029	CG	LEU	A	507	24.207	48.930	83.336	1.00 21.02
ATOM	4030	CD1	LEU	A	507	23.974	50.290	83.970	1.00 22.48
ATOM	4031	CD2	LEU	A	507	23.599	48.919	81.949	1.00 15.25
ATOM	4032	N	GLN	A	508	25.878	46.395	85.194	1.00 21.35
ATOM	4033	CA	GLN	A	508	25.215	45.333	85.979	1.00 18.08
ATOM	4034	C	GLN	A	508	25.386	45.561	87.508	1.00 34.24
ATOM	4035	O	GLN	A	508	24.653	45.017	88.343	1.00 34.04
ATOM	4036	CB	GLN	A	508	25.713	43.917	85.608	1.00 10.94
ATOM	4037	CG	GLN	A	508	25.366	43.446	84.191	1.00 26.42
ATOM	4038	CD	GLN	A	508	25.635	41.944	84.002	1.00 52.93
ATOM	4039	OE1	GLN	A	508	26.550	41.396	84.628	1.00 32.89
ATOM	4040	NE2	GLN	A	508	24.864	41.252	83.147	1.00 34.36
ATOM	4041	N	ARG	A	509	26.380	46.361	87.901	1.00 33.73
ATOM	4042	CA	ARG	A	509	26.600	46.614	89.328	1.00 32.53
ATOM	4043	C	ARG	A	509	26.153	48.016	89.727	1.00 33.63
ATOM	4044	O	ARG	A	509	26.509	48.522	90.777	1.00 31.08
ATOM	4045	CB	ARG	A	509	28.055	46.440	89.760	1.00 29.22
ATOM	4046	CG	ARG	A	509	28.553	45.014	89.733	1.00 29.78
ATOM	4047	CD	ARG	A	509	27.744	44.054	90.609	1.00 30.86
ATOM	4048	NE	ARG	A	509	28.533	43.602	91.756	1.00 82.23
ATOM	4049	CZ	ARG	A	509	29.842	43.274	91.726	1.00100.00
ATOM	4050	NH1	ARG	A	509	30.579	43.315	90.613	1.00 92.85
ATOM	4051	NH2	ARG	A	509	30.430	42.881	92.855	1.00 91.85
ATOM	4052	N	ALA	A	510	25.384	48.659	88.880	1.00 32.59
ATOM	4053	CA	ALA	A	510	24.952	49.985	89.215	1.00 32.51
ATOM	4054	C	ALA	A	510	24.151	49.845	90.479	1.00 34.97
ATOM	4055	O	ALA	A	510	23.601	48.785	90.693	1.00 37.57
ATOM	4056	CB	ALA	A	510	24.189	50.622	88.063	1.00 32.91
ATOM	4057	N	PRO	A	511	24.174	50.856	91.334	1.00 25.14
ATOM	4058	CA	PRO	A	511	24.867	52.102	91.052	1.00 21.00
ATOM	4059	C	PRO	A	511	26.217	52.178	91.694	1.00 29.23
ATOM	4060	O	PRO	A	511	26.445	51.601	92.723	1.00 28.16
ATOM	4061	CB	PRO	A	511	24.102	53.169	91.818	1.00 21.55
ATOM	4062	CG	PRO	A	511	23.316	52.432	92.886	1.00 28.68
ATOM	4063	CD	PRO	A	511	23.169	50.995	92.407	1.00 25.16
ATOM	4064	N	LEU	A	512	27.094	52.968	91.109	1.00 32.95
ATOM	4065	CA	LEU	A	512	28.394	53.188	91.686	1.00 33.42

ATOM	4066	C	LEU	A	512	28.287	54.512	92.397	1.00 38.65
ATOM	4067	O	LEU	A	512	27.388	55.305	92.114	1.00 40.69
ATOM	4068	CB	LEU	A	512	29.453	53.350	90.587	1.00 34.40
ATOM	4069	CG	LEU	A	512	30.178	52.049	90.216	1.00 40.13
ATOM	4070	CD1	LEU	A	512	29.222	51.086	89.508	1.00 39.04
ATOM	4071	CD2	LEU	A	512	31.322	52.385	89.273	1.00 44.61
ATOM	4072	N	PRO	A	513	29.196	54.781	93.312	1.00 31.05
ATOM	4073	CA	PRO	A	513	29.167	56.058	94.008	1.00 27.16
ATOM	4074	C	PRO	A	513	29.296	57.203	93.019	1.00 23.76
ATOM	4075	O	PRO	A	513	30.121	57.182	92.118	1.00 27.17
ATOM	4076	CB	PRO	A	513	30.387	56.013	94.948	1.00 25.59
ATOM	4077	CG	PRO	A	513	30.702	54.542	95.149	1.00 27.14
ATOM	4078	CD	PRO	A	513	30.030	53.779	94.032	1.00 25.00
ATOM	4079	N	LEU	A	514	28.478	58.203	93.185	1.00 22.92
ATOM	4080	CA	LEU	A	514	28.516	59.350	92.279	1.00 27.55
ATOM	4081	C	LEU	A	514	29.930	59.766	91.940	1.00 31.95
ATOM	4082	O	LEU	A	514	30.287	59.908	90.765	1.00 37.11
ATOM	4083	CB	LEU	A	514	27.673	60.564	92.741	1.00 30.03
ATOM	4084	CG	LEU	A	514	27.428	61.626	91.648	1.00 32.87
ATOM	4085	CD1	LEU	A	514	26.648	61.082	90.440	1.00 28.48
ATOM	4086	CD2	LEU	A	514	26.699	62.780	92.272	1.00 31.16
ATOM	4087	N	GLY	A	515	30.731	59.989	92.979	1.00 24.42
ATOM	4088	CA	GLY	A	515	32.131	60.384	92.811	1.00 25.59
ATOM	4089	C	GLY	A	515	32.902	59.472	91.835	1.00 33.83
ATOM	4090	O	GLY	A	515	33.746	59.914	91.035	1.00 35.67
ATOM	4091	N	HIS	A	516	32.602	58.180	91.891	1.00 26.40
ATOM	4092	CA	HIS	A	516	33.257	57.255	90.998	1.00 25.86
ATOM	4093	C	HIS	A	516	32.911	57.578	89.560	1.00 27.62
ATOM	4094	O	HIS	A	516	33.786	57.596	88.695	1.00 28.67
ATOM	4095	CB	HIS	A	516	32.826	55.814	91.282	1.00 25.39
ATOM	4096	CG	HIS	A	516	33.452	55.283	92.505	1.00 27.96
ATOM	4097	ND1	HIS	A	516	33.635	56.092	93.602	1.00 30.14
ATOM	4098	CD2	HIS	A	516	33.929	54.037	92.791	1.00 27.79
ATOM	4099	CE1	HIS	A	516	34.205	55.336	94.534	1.00 27.58
ATOM	4100	NE2	HIS	A	516	34.390	54.099	94.085	1.00 27.02
ATOM	4101	N	ILE	A	517	31.617	57.815	89.315	1.00 21.40
ATOM	4102	CA	ILE	A	517	31.137	58.107	87.973	1.00 22.75
ATOM	4103	C	ILE	A	517	31.706	59.424	87.462	1.00 31.09
ATOM	4104	O	ILE	A	517	32.246	59.558	86.352	1.00 28.78
ATOM	4105	CB	ILE	A	517	29.601	58.024	87.930	1.00 27.12
ATOM	4106	CG1	ILE	A	517	29.225	56.610	88.312	1.00 29.40
ATOM	4107	CG2	ILE	A	517	29.013	58.285	86.536	1.00 25.49
ATOM	4108	CD1	ILE	A	517	29.305	55.665	87.105	1.00 34.77
ATOM	4109	N	LYS	A	518	31.589	60.416	88.308	1.00 27.28
ATOM	4110	CA	LYS	A	518	32.108	61.690	87.955	1.00 23.77
ATOM	4111	C	LYS	A	518	33.558	61.482	87.485	1.00 24.03
ATOM	4112	O	LYS	A	518	33.982	61.831	86.391	1.00 26.08
ATOM	4113	CB	LYS	A	518	32.038	62.557	89.210	1.00 24.00
ATOM	4114	CG	LYS	A	518	30.641	63.060	89.591	1.00 19.24
ATOM	4115	CD	LYS	A	518	30.721	64.276	90.537	1.00 27.93
ATOM	4116	CE	LYS	A	518	29.379	64.877	90.962	1.00 37.11
ATOM	4117	NZ	LYS	A	518	28.924	65.988	90.104	1.00 52.30
ATOM	4118	N	ARG	A	519	34.322	60.899	88.361	1.00 17.90
ATOM	4119	CA	ARG	A	519	35.703	60.636	88.098	1.00 20.80
ATOM	4120	C	ARG	A	519	35.862	59.874	86.802	1.00 28.98
ATOM	4121	O	ARG	A	519	36.812	60.084	86.051	1.00 29.86
ATOM	4122	CB	ARG	A	519	36.313	59.844	89.276	1.00 20.56
ATOM	4123	CG	ARG	A	519	37.721	59.308	89.036	1.00 29.02
ATOM	4124	CD	ARG	A	519	38.668	60.320	88.404	1.00 41.17
ATOM	4125	NE	ARG	A	519	40.086	60.008	88.616	1.00 59.84
ATOM	4126	CZ	ARG	A	519	41.076	60.858	88.349	1.00 50.77
ATOM	4127	NH1	ARG	A	519	40.838	62.073	87.880	1.00 31.21
ATOM	4128	NH2	ARG	A	519	42.329	60.486	88.543	1.00 31.86
ATOM	4129	N	MET	A	520	34.937	58.956	86.565	1.00 25.08

ATOM	4130	CA	MET	A	520	34.979	58.121	85.379	1.00 24.56
ATOM	4131	C	MET	A	520	34.906	58.918	84.086	1.00 29.37
ATOM	4132	O	MET	A	520	35.651	58.687	83.114	1.00 27.92
ATOM	4133	CB	MET	A	520	33.905	57.007	85.442	1.00 26.98
ATOM	4134	CG	MET	A	520	34.082	55.902	84.399	1.00 28.02
ATOM	4135	SD	MET	A	520	32.830	54.591	84.479	1.00 27.87
ATOM	4136	CE	MET	A	520	33.246	53.825	86.070	1.00 22.09
ATOM	4137	N	GLN	A	521	33.982	59.864	84.067	1.00 28.32
ATOM	4138	CA	GLN	A	521	33.838	60.672	82.886	1.00 28.34
ATOM	4139	C	GLN	A	521	35.067	61.540	82.785	1.00 36.52
ATOM	4140	O	GLN	A	521	35.514	61.879	81.707	1.00 35.87
ATOM	4141	CB	GLN	A	521	32.514	61.451	82.863	1.00 28.34
ATOM	4142	CG	GLN	A	521	32.564	62.774	82.079	1.00 9.68
ATOM	4143	CD	GLN	A	521	32.890	62.572	80.616	1.00 27.55
ATOM	4144	OE1	GLN	A	521	33.382	63.491	79.924	1.00 28.25
ATOM	4145	NE2	GLN	A	521	32.657	61.368	80.142	1.00 25.70
ATOM	4146	N	GLU	A	522	35.626	61.827	83.963	1.00 36.19
ATOM	4147	CA	GLU	A	522	36.818	62.648	84.171	1.00 36.13
ATOM	4148	C	GLU	A	522	38.136	62.046	83.662	1.00 42.48
ATOM	4149	O	GLU	A	522	39.099	62.735	83.335	1.00 42.40
ATOM	4150	CB	GLU	A	522	36.857	63.035	85.641	1.00 37.79
ATOM	4151	CG	GLU	A	522	38.233	63.196	86.273	1.00 58.85
ATOM	4152	CD	GLU	A	522	38.046	64.040	87.493	1.00 73.64
ATOM	4153	OE1	GLU	A	522	37.006	64.641	87.709	1.00 45.66
ATOM	4154	OE2	GLU	A	522	39.081	64.037	88.289	1.00 47.91
ATOM	4155	N	VAL	A	523	38.188	60.739	83.552	1.00 40.13
ATOM	4156	CA	VAL	A	523	39.401	60.136	83.058	1.00 37.49
ATOM	4157	C	VAL	A	523	39.205	59.351	81.778	1.00 38.88
ATOM	4158	O	VAL	A	523	40.195	59.016	81.138	1.00 40.21
ATOM	4159	CB	VAL	A	523	40.184	59.370	84.102	1.00 40.01
ATOM	4160	CG1	VAL	A	523	40.231	60.165	85.413	1.00 39.12
ATOM	4161	CG2	VAL	A	523	39.534	58.017	84.320	1.00 39.82
ATOM	4162	N	TYR	A	524	37.952	59.048	81.379	1.00 30.35
ATOM	4163	CA	TYR	A	524	37.801	58.330	80.114	1.00 28.11
ATOM	4164	C	TYR	A	524	37.061	59.144	79.074	1.00 33.14
ATOM	4165	O	TYR	A	524	37.076	58.802	77.908	1.00 35.84
ATOM	4166	CB	TYR	A	524	37.281	56.878	80.119	1.00 25.56
ATOM	4167	CG	TYR	A	524	37.941	55.960	81.111	1.00 20.87
ATOM	4168	CD1	TYR	A	524	39.324	55.938	81.258	1.00 21.59
ATOM	4169	CD2	TYR	A	524	37.170	55.083	81.879	1.00 19.80
ATOM	4170	CE1	TYR	A	524	39.905	55.063	82.176	1.00 25.64
ATOM	4171	CE2	TYR	A	524	37.731	54.227	82.827	1.00 18.61
ATOM	4172	CZ	TYR	A	524	39.116	54.231	82.969	1.00 19.81
ATOM	4173	OH	TYR	A	524	39.706	53.402	83.863	1.00 23.92
ATOM	4174	N	ASN	A	525	36.416	60.221	79.496	1.00 25.98
ATOM	4175	CA	ASN	A	525	35.687	61.088	78.588	1.00 25.01
ATOM	4176	C	ASN	A	525	34.661	60.354	77.735	1.00 29.86
ATOM	4177	O	ASN	A	525	34.533	60.535	76.499	1.00 29.39
ATOM	4178	CB	ASN	A	525	36.637	61.922	77.739	1.00 29.55
ATOM	4179	CG	ASN	A	525	35.949	62.980	76.894	1.00 30.32
ATOM	4180	OD1	ASN	A	525	36.460	63.332	75.850	1.00 32.77
ATOM	4181	ND2	ASN	A	525	34.822	63.527	77.344	1.00 13.80
ATOM	4182	N	PHE	A	526	33.924	59.512	78.436	1.00 24.21
ATOM	4183	CA	PHE	A	526	32.900	58.745	77.807	1.00 25.14
ATOM	4184	C	PHE	A	526	31.846	59.631	77.214	1.00 31.74
ATOM	4185	O	PHE	A	526	31.161	59.241	76.272	1.00 34.99
ATOM	4186	CB	PHE	A	526	32.256	57.732	78.781	1.00 26.60
ATOM	4187	CG	PHE	A	526	33.115	56.499	78.978	1.00 23.82
ATOM	4188	CD1	PHE	A	526	34.017	56.080	78.000	1.00 25.00
ATOM	4189	CD2	PHE	A	526	33.031	55.767	80.159	1.00 21.74
ATOM	4190	CE1	PHE	A	526	34.783	54.927	78.173	1.00 27.63
ATOM	4191	CE2	PHE	A	526	33.817	54.634	80.370	1.00 25.42
ATOM	4192	CZ	PHE	A	526	34.683	54.202	79.364	1.00 25.28
ATOM	4193	N	ASN	A	527	31.689	60.815	77.760	1.00 28.22

ATOM	4194	CA	ASN	A	527	30.657	61.688	77.214	1.00 31.18
ATOM	4195	C	ASN	A	527	30.884	62.046	75.744	1.00 33.17
ATOM	4196	O	ASN	A	527	29.965	62.394	74.999	1.00 30.80
ATOM	4197	CB	ASN	A	527	30.479	62.967	78.052	1.00 36.41
ATOM	4198	CG	ASN	A	527	29.638	62.752	79.292	1.00 46.99
ATOM	4199	OD1	ASN	A	527	29.647	63.571	80.209	1.00 36.82
ATOM	4200	ND2	ASN	A	527	28.922	61.636	79.338	1.00 43.55
ATOM	4201	N	ALA	A	528	32.136	61.947	75.348	1.00 27.46
ATOM	4202	CA	ALA	A	528	32.581	62.278	74.005	1.00 26.48
ATOM	4203	C	ALA	A	528	32.335	61.188	72.950	1.00 32.09
ATOM	4204	O	ALA	A	528	32.420	61.404	71.753	1.00 32.09
ATOM	4205	CB	ALA	A	528	34.076	62.584	74.105	1.00 26.04
ATOM	4206	N	ILE	A	529	32.067	59.983	73.402	1.00 31.35
ATOM	4207	CA	ILE	A	529	31.854	58.859	72.529	1.00 28.47
ATOM	4208	C	ILE	A	529	30.492	58.904	71.887	1.00 35.96
ATOM	4209	O	ILE	A	529	29.486	59.023	72.578	1.00 38.79
ATOM	4210	CB	ILE	A	529	32.103	57.544	73.264	1.00 30.17
ATOM	4211	CG1	ILE	A	529	33.622	57.291	73.392	1.00 31.37
ATOM	4212	CG2	ILE	A	529	31.428	56.411	72.489	1.00 27.63
ATOM	4213	CD1	ILE	A	529	34.059	56.515	74.635	1.00 33.41
ATOM	4214	N	ASN	A	530	30.462	58.806	70.559	1.00 34.86
ATOM	4215	CA	ASN	A	530	29.196	58.841	69.852	1.00 36.44
ATOM	4216	C	ASN	A	530	28.596	57.495	69.473	1.00 39.90
ATOM	4217	O	ASN	A	530	27.452	57.437	69.043	1.00 41.37
ATOM	4218	CB	ASN	A	530	28.951	60.044	68.928	1.00 51.44
ATOM	4219	CG	ASN	A	530	28.461	61.253	69.732	1.00100.00
ATOM	4220	OD1	ASN	A	530	27.652	61.109	70.665	1.00100.00
ATOM	4221	ND2	ASN	A	530	28.955	62.442	69.392	1.00 91.39
ATOM	4222	N	ASN	A	531	29.368	56.403	69.688	1.00 30.37
ATOM	4223	CA	ASN	A	531	28.912	55.030	69.446	1.00 28.14
ATOM	4224	C	ASN	A	531	27.696	54.753	70.360	1.00 32.80
ATOM	4225	O	ASN	A	531	27.746	54.887	71.611	1.00 36.74
ATOM	4226	CB	ASN	A	531	30.092	54.066	69.690	1.00 24.31
ATOM	4227	CG	ASN	A	531	29.770	52.601	69.730	1.00 34.44
ATOM	4228	OD1	ASN	A	531	28.795	52.182	70.359	1.00 36.49
ATOM	4229	ND2	ASN	A	531	30.643	51.810	69.099	1.00 30.57
ATOM	4230	N	SER	A	532	26.570	54.403	69.734	1.00 22.02
ATOM	4231	CA	SER	A	532	25.325	54.183	70.459	1.00 19.67
ATOM	4232	C	SER	A	532	25.323	53.208	71.627	1.00 26.15
ATOM	4233	O	SER	A	532	24.767	53.475	72.680	1.00 26.64
ATOM	4234	CB	SER	A	532	24.090	54.034	69.582	1.00 26.92
ATOM	4235	OG	SER	A	532	24.294	53.211	68.452	1.00 23.59
ATOM	4236	N	GLU	A	533	25.929	52.062	71.423	1.00 22.68
ATOM	4237	CA	GLU	A	533	25.995	51.036	72.420	1.00 22.97
ATOM	4238	C	GLU	A	533	26.677	51.569	73.635	1.00 30.48
ATOM	4239	O	GLU	A	533	26.125	51.539	74.749	1.00 31.13
ATOM	4240	CB	GLU	A	533	26.683	49.779	71.850	1.00 23.96
ATOM	4241	CG	GLU	A	533	25.827	49.146	70.733	1.00 20.82
ATOM	4242	CD	GLU	A	533	24.611	48.450	71.276	1.00 40.65
ATOM	4243	OE1	GLU	A	533	24.432	48.256	72.476	1.00 36.25
ATOM	4244	OE2	GLU	A	533	23.782	48.038	70.339	1.00 25.87
ATOM	4245	N	ILE	A	534	27.872	52.101	73.392	1.00 26.20
ATOM	4246	CA	ILE	A	534	28.622	52.672	74.484	1.00 26.32
ATOM	4247	C	ILE	A	534	27.900	53.849	75.121	1.00 27.83
ATOM	4248	O	ILE	A	534	27.697	53.911	76.326	1.00 26.54
ATOM	4249	CB	ILE	A	534	30.051	53.022	74.102	1.00 29.16
ATOM	4250	CG1	ILE	A	534	30.738	51.808	73.479	1.00 29.47
ATOM	4251	CG2	ILE	A	534	30.801	53.458	75.353	1.00 28.28
ATOM	4252	CD1	ILE	A	534	32.038	52.184	72.765	1.00 34.99
ATOM	4253	N	ARG	A	535	27.480	54.805	74.320	1.00 24.30
ATOM	4254	CA	ARG	A	535	26.804	55.898	74.949	1.00 22.51
ATOM	4255	C	ARG	A	535	25.573	55.401	75.701	1.00 28.19
ATOM	4256	O	ARG	A	535	25.212	55.808	76.791	1.00 32.61
ATOM	4257	CB	ARG	A	535	26.457	56.942	73.913	1.00 24.83

ATOM	4258	CG	ARG	A	535	25.970	58.229	74.541	1.00	21.49
ATOM	4259	CD	ARG	A	535	25.327	59.183	73.554	1.00	13.79
ATOM	4260	NE	ARG	A	535	25.194	60.457	74.213	1.00	31.38
ATOM	4261	CZ	ARG	A	535	26.256	61.140	74.554	1.00	29.41
ATOM	4262	NH1	ARG	A	535	27.463	60.677	74.259	1.00	26.45
ATOM	4263	NH2	ARG	A	535	26.110	62.302	75.195	1.00	19.99
ATOM	4264	N	PHE	A	536	24.911	54.466	75.126	1.00	23.44
ATOM	4265	CA	PHE	A	536	23.740	53.980	75.770	1.00	22.05
ATOM	4266	C	PHE	A	536	23.976	53.555	77.199	1.00	22.74
ATOM	4267	O	PHE	A	536	23.349	54.113	78.105	1.00	22.06
ATOM	4268	CB	PHE	A	536	23.117	52.865	74.919	1.00	23.17
ATOM	4269	CG	PHE	A	536	22.040	52.153	75.658	1.00	21.92
ATOM	4270	CD1	PHE	A	536	20.933	52.845	76.150	1.00	22.66
ATOM	4271	CD2	PHE	A	536	22.145	50.783	75.882	1.00	23.25
ATOM	4272	CE1	PHE	A	536	19.926	52.181	76.847	1.00	21.23
ATOM	4273	CE2	PHE	A	536	21.147	50.101	76.576	1.00	24.70
ATOM	4274	CZ	PHE	A	536	20.047	50.811	77.065	1.00	20.57
ATOM	4275	N	ARG	A	537	24.863	52.560	77.364	1.00	18.22
ATOM	4276	CA	ARG	A	537	25.239	51.995	78.665	1.00	19.20
ATOM	4277	C	ARG	A	537	25.932	52.963	79.618	1.00	27.62
ATOM	4278	O	ARG	A	537	25.803	52.845	80.837	1.00	26.73
ATOM	4279	CB	ARG	A	537	26.035	50.709	78.556	1.00	18.91
ATOM	4280	CG	ARG	A	537	25.318	49.656	77.708	1.00	16.55
ATOM	4281	CD	ARG	A	537	26.181	48.426	77.387	1.00	21.58
ATOM	4282	NE	ARG	A	537	25.341	47.357	76.886	1.00	28.42
ATOM	4283	CZ	ARG	A	537	25.060	47.206	75.609	1.00	18.29
ATOM	4284	NH1	ARG	A	537	25.569	48.004	74.703	1.00	22.46
ATOM	4285	NH2	ARG	A	537	24.240	46.236	75.224	1.00	25.22
ATOM	4286	N	TRP	A	538	26.668	53.930	79.064	1.00	24.21
ATOM	4287	CA	TRP	A	538	27.337	54.918	79.867	1.00	22.11
ATOM	4288	C	TRP	A	538	26.274	55.719	80.550	1.00	28.09
ATOM	4289	O	TRP	A	538	26.320	55.951	81.741	1.00	27.39
ATOM	4290	CB	TRP	A	538	28.064	55.888	78.949	1.00	20.48
ATOM	4291	CG	TRP	A	538	28.606	57.157	79.580	1.00	21.29
ATOM	4292	CD1	TRP	A	538	28.641	58.345	78.968	1.00	22.86
ATOM	4293	CD2	TRP	A	538	29.286	57.352	80.845	1.00	21.79
ATOM	4294	NE1	TRP	A	538	29.228	59.270	79.769	1.00	22.70
ATOM	4295	CE2	TRP	A	538	29.643	58.696	80.911	1.00	24.79
ATOM	4296	CE3	TRP	A	538	29.574	56.535	81.946	1.00	23.35
ATOM	4297	CZ2	TRP	A	538	30.280	59.248	82.025	1.00	25.89
ATOM	4298	CZ3	TRP	A	538	30.203	57.056	83.046	1.00	23.35
ATOM	4299	CH2	TRP	A	538	30.562	58.405	83.081	1.00	24.89
ATOM	4300	N	LEU	A	539	25.303	56.161	79.758	1.00	27.31
ATOM	4301	CA	LEU	A	539	24.229	56.974	80.306	1.00	27.18
ATOM	4302	C	LEU	A	539	23.369	56.245	81.332	1.00	28.25
ATOM	4303	O	LEU	A	539	22.857	56.822	82.266	1.00	27.19
ATOM	4304	CB	LEU	A	539	23.428	57.812	79.262	1.00	26.37
ATOM	4305	CG	LEU	A	539	24.269	58.682	78.279	1.00	25.71
ATOM	4306	CD1	LEU	A	539	23.369	59.424	77.290	1.00	21.79
ATOM	4307	CD2	LEU	A	539	25.146	59.680	79.011	1.00	23.51
ATOM	4308	N	ARG	A	540	23.199	54.960	81.188	1.00	27.56
ATOM	4309	CA	ARG	A	540	22.390	54.283	82.170	1.00	26.88
ATOM	4310	C	ARG	A	540	23.145	54.229	83.453	1.00	31.82
ATOM	4311	O	ARG	A	540	22.618	54.448	84.539	1.00	32.72
ATOM	4312	CB	ARG	A	540	22.034	52.888	81.732	1.00	24.48
ATOM	4313	CG	ARG	A	540	21.447	52.885	80.331	1.00	32.96
ATOM	4314	CD	ARG	A	540	20.695	51.597	80.090	1.00	33.19
ATOM	4315	NE	ARG	A	540	19.660	51.414	81.085	1.00	33.95
ATOM	4316	CZ	ARG	A	540	19.151	50.242	81.409	1.00	30.83
ATOM	4317	NH1	ARG	A	540	19.564	49.132	80.849	1.00	25.37
ATOM	4318	NH2	ARG	A	540	18.186	50.186	82.317	1.00	30.30
ATOM	4319	N	LEU	A	541	24.414	53.948	83.318	1.00	28.93
ATOM	4320	CA	LEU	A	541	25.239	53.895	84.505	1.00	26.36
ATOM	4321	C	LEU	A	541	25.036	55.210	85.277	1.00	31.00

ATOM	4322	O	LEU	A	541	24.632	55.246	86.439	1.00 31.62
ATOM	4323	CB	LEU	A	541	26.702	53.586	84.094	1.00 23.61
ATOM	4324	CG	LEU	A	541	27.730	53.533	85.212	1.00 24.67
ATOM	4325	CD1	LEU	A	541	27.387	52.411	86.190	1.00 25.02
ATOM	4326	CD2	LEU	A	541	29.098	53.245	84.621	1.00 19.31
ATOM	4327	N	CYS	A	542	25.254	56.307	84.570	1.00 30.52
ATOM	4328	CA	CYS	A	542	25.115	57.661	85.105	1.00 31.76
ATOM	4329	C	CYS	A	542	23.808	57.996	85.805	1.00 32.71
ATOM	4330	O	CYS	A	542	23.801	58.536	86.914	1.00 33.97
ATOM	4331	CB	CYS	A	542	25.461	58.744	84.073	1.00 31.30
ATOM	4332	SG	CYS	A	542	27.085	58.488	83.347	1.00 34.39
ATOM	4333	N	ILE	A	543	22.711	57.708	85.125	1.00 25.61
ATOM	4334	CA	ILE	A	543	21.382	57.982	85.643	1.00 23.12
ATOM	4335	C	ILE	A	543	21.199	57.161	86.885	1.00 30.15
ATOM	4336	O	ILE	A	543	20.900	57.645	87.972	1.00 30.73
ATOM	4337	CB	ILE	A	543	20.340	57.627	84.585	1.00 23.75
ATOM	4338	CG1	ILE	A	543	20.369	58.664	83.468	1.00 24.09
ATOM	4339	CG2	ILE	A	543	18.955	57.572	85.182	1.00 22.99
ATOM	4340	CD1	ILE	A	543	20.386	60.109	83.982	1.00 27.34
ATOM	4341	N	GLN	A	544	21.440	55.884	86.695	1.00 27.99
ATOM	4342	CA	GLN	A	544	21.320	54.929	87.756	1.00 25.72
ATOM	4343	C	GLN	A	544	22.243	55.269	88.901	1.00 26.34
ATOM	4344	O	GLN	A	544	22.029	54.826	90.014	1.00 26.24
ATOM	4345	CB	GLN	A	544	21.562	53.512	87.210	1.00 26.76
ATOM	4346	CG	GLN	A	544	20.355	52.955	86.432	1.00 17.74
ATOM	4347	CD	GLN	A	544	20.598	51.604	85.743	1.00 32.62
ATOM	4348	OE1	GLN	A	544	20.326	51.432	84.551	1.00 38.66
ATOM	4349	NE2	GLN	A	544	21.063	50.627	86.494	1.00 14.93
ATOM	4350	N	SER	A	545	23.286	56.033	88.625	1.00 21.73
ATOM	4351	CA	SER	A	545	24.187	56.392	89.685	1.00 22.42
ATOM	4352	C	SER	A	545	23.819	57.726	90.287	1.00 33.67
ATOM	4353	O	SER	A	545	24.567	58.257	91.133	1.00 37.22
ATOM	4354	CB	SER	A	545	25.646	56.322	89.338	1.00 21.57
ATOM	4355	OG	SER	A	545	25.980	54.968	89.163	1.00 31.72
ATOM	4356	N	LYS	A	546	22.662	58.251	89.841	1.00 23.09
ATOM	4357	CA	LYS	A	546	22.135	59.490	90.356	1.00 20.79
ATOM	4358	C	LYS	A	546	22.887	60.738	89.961	1.00 27.55
ATOM	4359	O	LYS	A	546	23.001	61.655	90.771	1.00 27.95
ATOM	4360	CB	LYS	A	546	22.126	59.449	91.881	1.00 21.71
ATOM	4361	CG	LYS	A	546	21.498	58.195	92.484	1.00 15.90
ATOM	4362	CD	LYS	A	546	20.245	57.814	91.731	1.00 39.84
ATOM	4363	CE	LYS	A	546	19.355	56.850	92.498	1.00 45.16
ATOM	4364	NZ	LYS	A	546	18.197	56.399	91.704	1.00 40.14
ATOM	4365	N	TRP	A	547	23.414	60.776	88.753	1.00 23.26
ATOM	4366	CA	TRP	A	547	24.141	61.931	88.289	1.00 21.90
ATOM	4367	C	TRP	A	547	23.221	62.901	87.570	1.00 29.82
ATOM	4368	O	TRP	A	547	22.808	62.679	86.432	1.00 34.91
ATOM	4369	CB	TRP	A	547	25.262	61.500	87.361	1.00 21.04
ATOM	4370	CG	TRP	A	547	26.254	62.591	87.206	1.00 22.57
ATOM	4371	CD1	TRP	A	547	26.224	63.769	87.844	1.00 25.87
ATOM	4372	CD2	TRP	A	547	27.437	62.588	86.417	1.00 23.40
ATOM	4373	NE1	TRP	A	547	27.316	64.511	87.517	1.00 25.64
ATOM	4374	CE2	TRP	A	547	28.081	63.819	86.635	1.00 27.46
ATOM	4375	CE3	TRP	A	547	28.014	61.668	85.547	1.00 26.21
ATOM	4376	CZ2	TRP	A	547	29.279	64.162	85.995	1.00 27.44
ATOM	4377	CZ3	TRP	A	547	29.195	62.009	84.923	1.00 28.70
ATOM	4378	CH2	TRP	A	547	29.822	63.236	85.138	1.00 28.41
ATOM	4379	N	GLU	A	548	22.888	63.995	88.227	1.00 22.95
ATOM	4380	CA	GLU	A	548	21.979	64.970	87.649	1.00 20.70
ATOM	4381	C	GLU	A	548	22.419	65.473	86.305	1.00 28.32
ATOM	4382	O	GLU	A	548	21.598	65.735	85.391	1.00 29.41
ATOM	4383	CB	GLU	A	548	21.635	66.144	88.607	1.00 22.45
ATOM	4384	CG	GLU	A	548	20.884	65.709	89.919	1.00 30.56
ATOM	4385	CD	GLU	A	548	20.337	66.848	90.765	1.00 59.35

ATOM	4386	OE1	GLU	A	548	20.336	68.021	90.413	1.00	81.52
ATOM	4387	OE2	GLU	A	548	19.888	66.450	91.925	1.00	57.05
ATOM	4388	N	ASP	A	549	23.728	65.661	86.201	1.00	24.72
ATOM	4389	CA	ASP	A	549	24.276	66.190	84.981	1.00	21.48
ATOM	4390	C	ASP	A	549	23.914	65.359	83.795	1.00	30.08
ATOM	4391	O	ASP	A	549	23.760	65.869	82.697	1.00	32.05
ATOM	4392	CB	ASP	A	549	25.775	66.480	85.048	1.00	21.28
ATOM	4393	CG	ASP	A	549	26.076	67.463	86.130	1.00	37.74
ATOM	4394	OD1	ASP	A	549	25.432	68.479	86.297	1.00	48.21
ATOM	4395	OD2	ASP	A	549	27.076	67.115	86.882	1.00	46.51
ATOM	4396	N	ALA	A	550	23.766	64.073	84.032	1.00	27.68
ATOM	4397	CA	ALA	A	550	23.445	63.133	82.965	1.00	26.74
ATOM	4398	C	ALA	A	550	22.019	63.171	82.431	1.00	32.35
ATOM	4399	O	ALA	A	550	21.745	62.615	81.361	1.00	31.95
ATOM	4400	CB	ALA	A	550	23.812	61.713	83.372	1.00	25.48
ATOM	4401	N	ILE	A	551	21.123	63.795	83.192	1.00	28.71
ATOM	4402	CA	ILE	A	551	19.716	63.882	82.832	1.00	28.20
ATOM	4403	C	ILE	A	551	19.461	64.355	81.411	1.00	32.04
ATOM	4404	O	ILE	A	551	18.833	63.679	80.619	1.00	31.75
ATOM	4405	CB	ILE	A	551	18.876	64.641	83.868	1.00	30.29
ATOM	4406	CG1	ILE	A	551	19.038	63.985	85.226	1.00	31.50
ATOM	4407	CG2	ILE	A	551	17.391	64.661	83.475	1.00	24.75
ATOM	4408	CD1	ILE	A	551	18.072	64.561	86.253	1.00	31.62
ATOM	4409	N	PRO	A	552	19.969	65.529	81.099	1.00	33.75
ATOM	4410	CA	PRO	A	552	19.793	66.121	79.796	1.00	32.60
ATOM	4411	C	PRO	A	552	20.240	65.224	78.669	1.00	30.34
ATOM	4412	O	PRO	A	552	19.583	65.119	77.622	1.00	27.23
ATOM	4413	CB	PRO	A	552	20.659	67.383	79.787	1.00	34.45
ATOM	4414	CG	PRO	A	552	21.348	67.500	81.139	1.00	38.39
ATOM	4415	CD	PRO	A	552	20.934	66.296	81.950	1.00	34.48
ATOM	4416	N	LEU	A	553	21.391	64.616	78.891	1.00	23.74
ATOM	4417	CA	LEU	A	553	21.997	63.727	77.931	1.00	22.72
ATOM	4418	C	LEU	A	553	21.138	62.522	77.670	1.00	32.68
ATOM	4419	O	LEU	A	553	21.015	62.087	76.523	1.00	35.70
ATOM	4420	CB	LEU	A	553	23.362	63.281	78.439	1.00	21.57
ATOM	4421	CG	LEU	A	553	24.196	64.496	78.818	1.00	24.02
ATOM	4422	CD1	LEU	A	553	25.608	64.071	79.174	1.00	19.59
ATOM	4423	CD2	LEU	A	553	24.188	65.479	77.630	1.00	18.60
ATOM	4424	N	ALA	A	554	20.563	61.973	78.754	1.00	30.05
ATOM	4425	CA	ALA	A	554	19.726	60.779	78.669	1.00	27.72
ATOM	4426	C	ALA	A	554	18.432	61.107	77.988	1.00	36.03
ATOM	4427	O	ALA	A	554	17.944	60.332	77.163	1.00	37.08
ATOM	4428	CB	ALA	A	554	19.475	60.165	80.017	1.00	26.78
ATOM	4429	N	LEU	A	555	17.898	62.283	78.320	1.00	29.70
ATOM	4430	CA	LEU	A	555	16.644	62.724	77.720	1.00	28.32
ATOM	4431	C	LEU	A	555	16.803	62.902	76.229	1.00	29.19
ATOM	4432	O	LEU	A	555	15.970	62.506	75.385	1.00	26.13
ATOM	4433	CB	LEU	A	555	16.110	64.027	78.342	1.00	28.26
ATOM	4434	CG	LEU	A	555	15.371	63.814	79.666	1.00	32.76
ATOM	4435	CD1	LEU	A	555	15.360	65.118	80.464	1.00	34.66
ATOM	4436	CD2	LEU	A	555	13.938	63.334	79.427	1.00	27.50
ATOM	4437	N	LYS	A	556	17.922	63.524	75.950	1.00	28.45
ATOM	4438	CA	LYS	A	556	18.325	63.839	74.615	1.00	28.76
ATOM	4439	C	LYS	A	556	18.369	62.591	73.800	1.00	35.11
ATOM	4440	O	LYS	A	556	17.670	62.491	72.796	1.00	41.80
ATOM	4441	CB	LYS	A	556	19.645	64.592	74.599	1.00	31.79
ATOM	4442	CG	LYS	A	556	20.101	65.139	73.250	1.00	63.55
ATOM	4443	CD	LYS	A	556	21.585	65.518	73.254	1.00	81.77
ATOM	4444	CE	LYS	A	556	22.046	66.270	72.011	1.00	79.68
ATOM	4445	NZ	LYS	A	556	23.239	65.661	71.401	1.00	73.00
ATOM	4446	N	MET	A	557	19.154	61.623	74.248	1.00	26.96
ATOM	4447	CA	MET	A	557	19.305	60.364	73.514	1.00	23.97
ATOM	4448	C	MET	A	557	18.033	59.553	73.287	1.00	30.96
ATOM	4449	O	MET	A	557	17.811	58.907	72.263	1.00	23.24

ATOM	4450	CB	MET	A	557	20.401	59.488	74.104	1.00 24.89
ATOM	4451	CG	MET	A	557	20.533	58.163	73.368	1.00 29.37
ATOM	4452	SD	MET	A	557	22.029	57.276	73.864	1.00 33.21
ATOM	4453	CE	MET	A	557	21.939	55.812	72.793	1.00 30.16
ATOM	4454	N	ALA	A	558	17.203	59.568	74.287	1.00 33.42
ATOM	4455	CA	ALA	A	558	16.000	58.816	74.194	1.00 33.03
ATOM	4456	C	ALA	A	558	15.042	59.345	73.163	1.00 38.12
ATOM	4457	O	ALA	A	558	14.349	58.568	72.543	1.00 37.09
ATOM	4458	CB	ALA	A	558	15.317	58.780	75.553	1.00 32.89
ATOM	4459	N	THR	A	559	14.994	60.665	73.032	1.00 36.76
ATOM	4460	CA	THR	A	559	14.067	61.326	72.144	1.00 36.43
ATOM	4461	C	THR	A	559	14.588	61.590	70.794	1.00 41.71
ATOM	4462	O	THR	A	559	13.788	61.768	69.891	1.00 44.66
ATOM	4463	CB	THR	A	559	13.615	62.705	72.694	1.00 43.70
ATOM	4464	OG1	THR	A	559	14.728	63.545	72.957	1.00 38.88
ATOM	4465	CG2	THR	A	559	12.764	62.549	73.942	1.00 44.95
ATOM	4466	N	GLU	A	560	15.897	61.695	70.674	1.00 37.38
ATOM	4467	CA	GLU	A	560	16.495	62.018	69.395	1.00 36.51
ATOM	4468	C	GLU	A	560	16.652	60.846	68.448	1.00 40.11
ATOM	4469	O	GLU	A	560	17.003	61.052	67.300	1.00 43.23
ATOM	4470	CB	GLU	A	560	17.799	62.820	69.519	1.00 38.13
ATOM	4471	CG	GLU	A	560	17.653	64.142	70.292	1.00 54.29
ATOM	4472	CD	GLU	A	560	18.857	65.043	70.127	1.00 78.42
ATOM	4473	OE1	GLU	A	560	19.960	64.639	69.812	1.00 32.69
ATOM	4474	OE2	GLU	A	560	18.593	66.303	70.380	1.00 85.90
ATOM	4475	N	GLN	A	561	16.425	59.627	68.955	1.00 30.45
ATOM	4476	CA	GLN	A	561	16.467	58.356	68.230	1.00 22.57
ATOM	4477	C	GLN	A	561	15.398	57.523	68.878	1.00 26.95
ATOM	4478	O	GLN	A	561	14.978	57.814	69.975	1.00 27.79
ATOM	4479	CB	GLN	A	561	17.829	57.661	68.128	1.00 20.64
ATOM	4480	CG	GLN	A	561	18.470	57.290	69.491	1.00 22.59
ATOM	4481	CD	GLN	A	561	17.802	56.121	70.184	1.00 28.22
ATOM	4482	OE1	GLN	A	561	17.524	56.156	71.400	1.00 37.44
ATOM	4483	NE2	GLN	A	561	17.556	55.069	69.419	1.00 31.92
ATOM	4484	N	GLY	A	562	14.888	56.535	68.209	1.00 26.16
ATOM	4485	CA	GLY	A	562	13.801	55.810	68.858	1.00 27.83
ATOM	4486	C	GLY	A	562	13.932	54.320	68.761	1.00 41.56
ATOM	4487	O	GLY	A	562	12.936	53.614	68.677	1.00 45.37
ATOM	4488	N	ARG	A	563	15.171	53.864	68.742	1.00 37.40
ATOM	4489	CA	ARG	A	563	15.457	52.453	68.689	1.00 34.41
ATOM	4490	C	ARG	A	563	15.121	51.939	70.109	1.00 39.48
ATOM	4491	O	ARG	A	563	15.832	52.221	71.087	1.00 40.29
ATOM	4492	CB	ARG	A	563	16.932	52.231	68.284	1.00 18.23
ATOM	4493	CG	ARG	A	563	17.309	50.755	68.169	1.00 20.07
ATOM	4494	CD	ARG	A	563	18.779	50.514	68.512	1.00 25.07
ATOM	4495	NE	ARG	A	563	19.234	49.139	68.320	1.00 25.66
ATOM	4496	CZ	ARG	A	563	20.425	48.891	67.821	1.00 26.35
ATOM	4497	NH1	ARG	A	563	21.257	49.860	67.430	1.00 12.96
ATOM	4498	NH2	ARG	A	563	20.804	47.636	67.656	1.00 30.31
ATOM	4499	N	MET	A	564	13.989	51.228	70.239	1.00 33.12
ATOM	4500	CA	MET	A	564	13.487	50.695	71.526	1.00 31.84
ATOM	4501	C	MET	A	564	14.565	50.247	72.532	1.00 31.42
ATOM	4502	O	MET	A	564	14.494	50.501	73.744	1.00 25.72
ATOM	4503	CB	MET	A	564	12.323	49.682	71.365	1.00 32.45
ATOM	4504	CG	MET	A	564	11.196	50.225	70.487	1.00 35.78
ATOM	4505	SD	MET	A	564	9.695	49.205	70.533	1.00 40.85
ATOM	4506	CE	MET	A	564	10.177	47.892	69.382	1.00 35.87
ATOM	4507	N	LYS	A	565	15.562	49.581	71.966	1.00 31.68
ATOM	4508	CA	LYS	A	565	16.699	49.041	72.668	1.00 29.04
ATOM	4509	C	LYS	A	565	17.281	50.089	73.562	1.00 26.36
ATOM	4510	O	LYS	A	565	17.648	49.782	74.673	1.00 21.19
ATOM	4511	CB	LYS	A	565	17.747	48.494	71.697	1.00 29.06
ATOM	4512	CG	LYS	A	565	18.864	47.715	72.359	1.00 23.89
ATOM	4513	CD	LYS	A	565	19.982	47.355	71.392	1.00 35.75

ATOM	4514	CE	LYS	A	565	20.796	46.153	71.842	1.00 36.31
ATOM	4515	NZ	LYS	A	565	22.233	46.311	71.577	1.00 44.91
ATOM	4516	N	PHE	A	566	17.321	51.321	73.073	1.00 22.91
ATOM	4517	CA	PHE	A	566	17.866	52.423	73.833	1.00 24.36
ATOM	4518	C	PHE	A	566	16.814	53.253	74.571	1.00 30.37
ATOM	4519	O	PHE	A	566	16.882	53.540	75.758	1.00 30.52
ATOM	4520	CB	PHE	A	566	18.622	53.355	72.857	1.00 25.26
ATOM	4521	CG	PHE	A	566	19.738	52.677	72.088	1.00 24.09
ATOM	4522	CD1	PHE	A	566	20.392	51.559	72.609	1.00 23.51
ATOM	4523	CD2	PHE	A	566	20.165	53.187	70.858	1.00 24.48
ATOM	4524	CE1	PHE	A	566	21.432	50.958	71.900	1.00 23.73
ATOM	4525	CE2	PHE	A	566	21.211	52.620	70.129	1.00 24.75
ATOM	4526	CZ	PHE	A	566	21.828	51.491	70.668	1.00 25.20
ATOM	4527	N	THR	A	567	15.860	53.679	73.801	1.00 31.17
ATOM	4528	CA	THR	A	567	14.783	54.533	74.239	1.00 31.74
ATOM	4529	C	THR	A	567	13.985	54.037	75.458	1.00 33.79
ATOM	4530	O	THR	A	567	13.657	54.818	76.373	1.00 26.01
ATOM	4531	CB	THR	A	567	13.895	54.892	73.017	1.00 36.51
ATOM	4532	OG1	THR	A	567	14.527	55.844	72.138	1.00 24.12
ATOM	4533	CG2	THR	A	567	12.522	55.361	73.473	1.00 34.94
ATOM	4534	N	ARG	A	568	13.663	52.726	75.469	1.00 30.74
ATOM	4535	CA	ARG	A	568	12.864	52.166	76.545	1.00 26.30
ATOM	4536	C	ARG	A	568	13.486	52.226	77.882	1.00 28.61
ATOM	4537	O	ARG	A	568	12.876	52.667	78.832	1.00 30.84
ATOM	4538	CB	ARG	A	568	12.315	50.798	76.251	1.00 18.11
ATOM	4539	CG	ARG	A	568	11.342	50.919	75.088	1.00 29.19
ATOM	4540	CD	ARG	A	568	10.550	49.660	74.799	1.00 19.19
ATOM	4541	NE	ARG	A	568	9.707	49.343	75.917	1.00 28.72
ATOM	4542	CZ	ARG	A	568	9.254	48.138	76.133	1.00 32.39
ATOM	4543	NH1	ARG	A	568	9.528	47.144	75.291	1.00 29.79
ATOM	4544	NH2	ARG	A	568	8.507	47.930	77.208	1.00 16.44
ATOM	4545	N	PRO	A	569	14.705	51.774	77.925	1.00 28.41
ATOM	4546	CA	PRO	A	569	15.447	51.709	79.154	1.00 28.01
ATOM	4547	C	PRO	A	569	15.890	53.042	79.663	1.00 32.18
ATOM	4548	O	PRO	A	569	15.974	53.256	80.869	1.00 29.25
ATOM	4549	CB	PRO	A	569	16.607	50.732	78.919	1.00 28.83
ATOM	4550	CG	PRO	A	569	16.330	50.034	77.592	1.00 32.42
ATOM	4551	CD	PRO	A	569	15.234	50.829	76.893	1.00 29.82
ATOM	4552	N	LEU	A	570	16.143	53.949	78.741	1.00 31.95
ATOM	4553	CA	LEU	A	570	16.560	55.270	79.160	1.00 35.11
ATOM	4554	C	LEU	A	570	15.407	55.962	79.897	1.00 36.24
ATOM	4555	O	LEU	A	570	15.532	56.506	81.028	1.00 34.02
ATOM	4556	CB	LEU	A	570	17.021	56.110	77.932	1.00 37.06
ATOM	4557	CG	LEU	A	570	18.387	55.701	77.343	1.00 41.39
ATOM	4558	CD1	LEU	A	570	18.678	56.462	76.050	1.00 41.06
ATOM	4559	CD2	LEU	A	570	19.497	55.984	78.353	1.00 37.42
ATOM	4560	N	PHE	A	571	14.262	55.944	79.211	1.00 30.06
ATOM	4561	CA	PHE	A	571	13.084	56.541	79.758	1.00 27.27
ATOM	4562	C	PHE	A	571	12.813	55.899	81.095	1.00 25.94
ATOM	4563	O	PHE	A	571	12.399	56.536	82.030	1.00 27.16
ATOM	4564	CB	PHE	A	571	11.888	56.375	78.828	1.00 27.60
ATOM	4565	CG	PHE	A	571	11.546	57.616	78.042	1.00 27.70
ATOM	4566	CD1	PHE	A	571	11.193	58.820	78.651	1.00 29.97
ATOM	4567	CD2	PHE	A	571	11.557	57.570	76.651	1.00 28.87
ATOM	4568	CE1	PHE	A	571	10.861	59.953	77.910	1.00 28.24
ATOM	4569	CE2	PHE	A	571	11.233	58.684	75.886	1.00 30.43
ATOM	4570	CZ	PHE	A	571	10.877	59.875	76.520	1.00 29.55
ATOM	4571	N	LYS	A	572	13.089	54.618	81.196	1.00 22.77
ATOM	4572	CA	LYS	A	572	12.845	53.946	82.468	1.00 25.43
ATOM	4573	C	LYS	A	572	13.783	54.425	83.561	1.00 34.48
ATOM	4574	O	LYS	A	572	13.351	54.920	84.602	1.00 35.11
ATOM	4575	CB	LYS	A	572	12.736	52.428	82.392	1.00 26.89
ATOM	4576	CG	LYS	A	572	11.303	51.911	82.326	1.00 44.03
ATOM	4577	CD	LYS	A	572	11.219	50.426	81.922	1.00 57.87

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ATOM   4578  CE  LYS A 572      10.975  50.204  80.422  1.00 65.25
ATOM   4579  NZ  LYS A 572      11.535  48.954  79.850  1.00 61.06
ATOM   4580  N   ASP A 573      15.074  54.292  83.319  1.00 31.94
ATOM   4581  CA  ASP A 573      16.032  54.751  84.291  1.00 30.55
ATOM   4582  C   ASP A 573      15.684  56.166  84.712  1.00 32.26
ATOM   4583  O   ASP A 573      15.693  56.453  85.895  1.00 31.85
ATOM   4584  CB  ASP A 573      17.453  54.788  83.718  1.00 32.87
ATOM   4585  CG  ASP A 573      18.051  53.443  83.487  1.00 33.43
ATOM   4586  OD1 ASP A 573      17.517  52.422  83.853  1.00 29.11
ATOM   4587  OD2 ASP A 573      19.206  53.501  82.864  1.00 35.22
ATOM   4588  N   LEU A 574      15.387  57.071  83.745  1.00 29.50
ATOM   4589  CA  LEU A 574      15.062  58.461  84.109  1.00 27.65
ATOM   4590  C   LEU A 574      13.887  58.577  85.075  1.00 32.88
ATOM   4591  O   LEU A 574      13.864  59.411  85.962  1.00 31.04
ATOM   4592  CB  LEU A 574      14.844  59.385  82.909  1.00 26.24
ATOM   4593  CG  LEU A 574      16.068  59.567  82.027  1.00 30.41
ATOM   4594  CD1 LEU A 574      15.644  59.922  80.582  1.00 28.47
ATOM   4595  CD2 LEU A 574      16.974  60.659  82.604  1.00 27.06
ATOM   4596  N   ALA A 575      12.895  57.723  84.874  1.00 32.80
ATOM   4597  CA  ALA A 575      11.709  57.713  85.711  1.00 31.11
ATOM   4598  C   ALA A 575      12.002  57.140  87.083  1.00 35.71
ATOM   4599  O   ALA A 575      11.309  57.362  88.055  1.00 39.91
ATOM   4600  CB  ALA A 575      10.631  56.890  85.024  1.00 30.56
ATOM   4601  N   ALA A 576      13.049  56.364  87.170  1.00 28.55
ATOM   4602  CA  ALA A 576      13.390  55.778  88.448  1.00 22.80
ATOM   4603  C   ALA A 576      14.258  56.724  89.266  1.00 26.93
ATOM   4604  O   ALA A 576      14.444  56.591  90.461  1.00 30.45
ATOM   4605  CB  ALA A 576      14.023  54.415  88.245  1.00 20.31
ATOM   4606  N   PHE A 577      14.787  57.686  88.584  1.00 22.86
ATOM   4607  CA  PHE A 577      15.604  58.673  89.194  1.00 22.71
ATOM   4608  C   PHE A 577      14.651  59.751  89.673  1.00 32.25
ATOM   4609  O   PHE A 577      13.930  60.334  88.863  1.00 34.17
ATOM   4610  CB  PHE A 577      16.640  59.188  88.154  1.00 22.89
ATOM   4611  CG  PHE A 577      17.704  60.076  88.741  1.00 23.16
ATOM   4612  CD1 PHE A 577      17.847  60.231  90.120  1.00 26.60
ATOM   4613  CD2 PHE A 577      18.561  60.806  87.914  1.00 23.46
ATOM   4614  CE1 PHE A 577      18.818  61.082  90.661  1.00 27.55
ATOM   4615  CE2 PHE A 577      19.543  61.657  88.431  1.00 23.88
ATOM   4616  CZ  PHE A 577      19.669  61.791  89.813  1.00 23.59
ATOM   4617  N   ASP A 578      14.625  60.008  90.990  1.00 29.70
ATOM   4618  CA  ASP A 578      13.717  61.018  91.533  1.00 28.65
ATOM   4619  C   ASP A 578      13.862  62.357  90.881  1.00 28.55
ATOM   4620  O   ASP A 578      12.877  63.004  90.599  1.00 32.65
ATOM   4621  CB  ASP A 578      13.804  61.192  93.055  1.00 32.60
ATOM   4622  CG  ASP A 578      15.153  61.647  93.550  1.00 53.21
ATOM   4623  OD1 ASP A 578      16.175  61.594  92.872  1.00 51.81
ATOM   4624  OD2 ASP A 578      15.104  62.072  94.796  1.00 64.93
ATOM   4625  N   LYS A 579      15.104  62.750  90.674  1.00 20.12
ATOM   4626  CA  LYS A 579      15.470  64.012  90.084  1.00 21.01
ATOM   4627  C   LYS A 579      14.934  64.270  88.697  1.00 30.25
ATOM   4628  O   LYS A 579      14.620  65.413  88.368  1.00 35.12
ATOM   4629  CB  LYS A 579      16.982  64.223  90.104  1.00 24.11
ATOM   4630  CG  LYS A 579      17.552  64.202  91.512  1.00 48.98
ATOM   4631  CD  LYS A 579      17.252  65.488  92.286  1.00 76.92
ATOM   4632  CE  LYS A 579      16.495  65.258  93.588  1.00 87.93
ATOM   4633  NZ  LYS A 579      17.282  64.550  94.611  1.00 89.56
ATOM   4634  N   SER A 580      14.838  63.244  87.857  1.00 28.66
ATOM   4635  CA  SER A 580      14.368  63.437  86.459  1.00 28.56
ATOM   4636  C   SER A 580      13.007  62.829  86.129  1.00 32.95
ATOM   4637  O   SER A 580      12.561  62.870  84.992  1.00 35.30
ATOM   4638  CB  SER A 580      15.337  62.774  85.517  1.00 25.69
ATOM   4639  OG  SER A 580      15.476  61.424  85.969  1.00 25.12
ATOM   4640  N   HIS A 581      12.364  62.230  87.098  1.00 26.81
ATOM   4641  CA  HIS A 581      11.100  61.595  86.850  1.00 28.26
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ATOM   4642  C   HIS A 581      10.067  62.399  86.042  1.00 36.50
ATOM   4643  O   HIS A 581       9.644  62.031  84.927  1.00 34.71
ATOM   4644  CB  HIS A 581      10.553  61.047  88.152  1.00 29.76
ATOM   4645  CG  HIS A 581       9.148  60.588  87.968  1.00 35.31
ATOM   4646  ND1 HIS A 581       8.111  61.494  87.899  1.00 38.92
ATOM   4647  CD2 HIS A 581       8.634  59.338  87.891  1.00 36.84
ATOM   4648  CE1 HIS A 581       6.999  60.783  87.817  1.00 38.85
ATOM   4649  NE2 HIS A 581       7.280  59.488  87.734  1.00 38.13
ATOM   4650  N   ASP A 582       9.656  63.502  86.639  1.00 35.79
ATOM   4651  CA  ASP A 582       8.680  64.388  86.064  1.00 34.39
ATOM   4652  C   ASP A 582       9.035  64.807  84.659  1.00 37.82
ATOM   4653  O   ASP A 582       8.220  64.704  83.735  1.00 37.01
ATOM   4654  CB  ASP A 582       8.428  65.552  87.001  1.00 36.57
ATOM   4655  CG  ASP A 582       7.597  65.110  88.167  1.00 58.09
ATOM   4656  OD1 ASP A 582       6.708  64.289  88.070  1.00 63.17
ATOM   4657  OD2 ASP A 582       7.920  65.708  89.279  1.00 73.96
ATOM   4658  N   GLN A 583      10.272  65.255  84.488  1.00 32.88
ATOM   4659  CA  GLN A 583      10.750  65.648  83.169  1.00 29.92
ATOM   4660  C   GLN A 583      10.690  64.464  82.168  1.00 37.12
ATOM   4661  O   GLN A 583      10.362  64.624  80.990  1.00 37.42
ATOM   4662  CB  GLN A 583      12.172  66.182  83.287  1.00 28.54
ATOM   4663  CG  GLN A 583      12.704  66.648  81.929  1.00 48.12
ATOM   4664  CD  GLN A 583      13.957  67.475  82.081  1.00 64.09
ATOM   4665  OE1 GLN A 583      14.736  67.248  83.015  1.00 59.43
ATOM   4666  NE2 GLN A 583      14.130  68.461  81.201  1.00 55.34
ATOM   4667  N   ALA A 584      11.009  63.250  82.638  1.00 33.22
ATOM   4668  CA  ALA A 584      10.964  62.062  81.780  1.00 32.22
ATOM   4669  C   ALA A 584       9.557  61.841  81.315  1.00 37.45
ATOM   4670  O   ALA A 584       9.319  61.526  80.152  1.00 40.05
ATOM   4671  CB  ALA A 584      11.389  60.793  82.504  1.00 31.62
ATOM   4672  N   VAL A 585       8.622  61.995  82.261  1.00 30.42
ATOM   4673  CA  VAL A 585       7.217  61.806  81.946  1.00 29.16
ATOM   4674  C   VAL A 585       6.647  62.909  81.024  1.00 36.53
ATOM   4675  O   VAL A 585       5.933  62.690  80.052  1.00 36.22
ATOM   4676  CB  VAL A 585       6.408  61.567  83.209  1.00 29.78
ATOM   4677  CG1 VAL A 585       4.959  61.947  82.955  1.00 30.03
ATOM   4678  CG2 VAL A 585       6.464  60.085  83.539  1.00 27.82
ATOM   4679  N   ARG A 586       7.000  64.123  81.333  1.00 35.76
ATOM   4680  CA  ARG A 586       6.574  65.242  80.562  1.00 36.20
ATOM   4681  C   ARG A 586       7.146  65.125  79.180  1.00 44.65
ATOM   4682  O   ARG A 586       6.459  65.355  78.197  1.00 48.32
ATOM   4683  CB  ARG A 586       7.116  66.498  81.208  1.00 38.13
ATOM   4684  CG  ARG A 586       6.744  67.799  80.518  1.00 61.01
ATOM   4685  CD  ARG A 586       7.077  69.029  81.354  1.00 73.03
ATOM   4686  NE  ARG A 586       8.491  69.128  81.711  1.00 86.05
ATOM   4687  CZ  ARG A 586       8.961  69.001  82.957  1.00 98.46
ATOM   4688  NH1 ARG A 586       8.167  68.741  84.004  1.00 79.75
ATOM   4689  NH2 ARG A 586      10.268  69.103  83.159  1.00 77.55
ATOM   4690  N   THR A 587       8.426  64.769  79.110  1.00 39.49
ATOM   4691  CA  THR A 587       9.099  64.646  77.822  1.00 36.80
ATOM   4692  C   THR A 587       8.387  63.690  76.869  1.00 37.11
ATOM   4693  O   THR A 587       8.229  63.931  75.678  1.00 36.91
ATOM   4694  CB  THR A 587      10.634  64.384  77.917  1.00 39.40
ATOM   4695  OG1 THR A 587      11.303  65.334  78.717  1.00 46.27
ATOM   4696  CG2 THR A 587      11.233  64.460  76.529  1.00 32.60
ATOM   4697  N   TYR A 588       7.934  62.587  77.393  1.00 33.33
ATOM   4698  CA  TYR A 588       7.252  61.639  76.555  1.00 33.94
ATOM   4699  C   TYR A 588       5.890  62.146  76.090  1.00 37.02
ATOM   4700  O   TYR A 588       5.428  61.880  74.988  1.00 41.55
ATOM   4701  CB  TYR A 588       7.042  60.383  77.396  1.00 33.96
ATOM   4702  CG  TYR A 588       6.017  59.440  76.851  1.00 33.08
ATOM   4703  CD1 TYR A 588       6.331  58.640  75.754  1.00 35.64
ATOM   4704  CD2 TYR A 588       4.758  59.288  77.437  1.00 34.09
ATOM   4705  CE1 TYR A 588       5.424  57.703  75.251  1.00 34.36
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ATOM	4706	CE2	TYR	A	588	3.822	58.378	76.932	1.00 34.05
ATOM	4707	CZ	TYR	A	588	4.162	57.581	75.834	1.00 33.89
ATOM	4708	OH	TYR	A	588	3.275	56.674	75.322	1.00 23.43
ATOM	4709	N	GLN	A	589	5.216	62.853	76.959	1.00 25.04
ATOM	4710	CA	GLN	A	589	3.914	63.339	76.612	1.00 21.41
ATOM	4711	C	GLN	A	589	3.992	64.304	75.481	1.00 28.78
ATOM	4712	O	GLN	A	589	3.099	64.410	74.678	1.00 31.24
ATOM	4713	CB	GLN	A	589	3.241	63.935	77.832	1.00 21.73
ATOM	4714	CG	GLN	A	589	2.878	62.820	78.827	1.00 22.30
ATOM	4715	CD	GLN	A	589	1.695	62.069	78.293	1.00 52.83
ATOM	4716	OE1	GLN	A	589	1.511	62.003	77.075	1.00 60.15
ATOM	4717	NE2	GLN	A	589	0.864	61.542	79.182	1.00 53.04
ATOM	4718	N	GLU	A	590	5.099	65.001	75.409	1.00 28.36
ATOM	4719	CA	GLU	A	590	5.276	65.966	74.355	1.00 26.87
ATOM	4720	C	GLU	A	590	5.840	65.338	73.140	1.00 35.10
ATOM	4721	O	GLU	A	590	6.096	66.059	72.171	1.00 40.28
ATOM	4722	CB	GLU	A	590	6.323	67.011	74.747	1.00 27.61
ATOM	4723	CG	GLU	A	590	5.846	67.954	75.847	1.00 44.11
ATOM	4724	CD	GLU	A	590	6.981	68.759	76.388	1.00 75.35
ATOM	4725	OE1	GLU	A	590	8.120	68.689	75.925	1.00 54.78
ATOM	4726	OE2	GLU	A	590	6.609	69.516	77.403	1.00 59.46
ATOM	4727	N	HIS	A	591	6.091	64.031	73.207	1.00 27.57
ATOM	4728	CA	HIS	A	591	6.713	63.384	72.086	1.00 25.58
ATOM	4729	C	HIS	A	591	5.928	62.249	71.578	1.00 32.34
ATOM	4730	O	HIS	A	591	6.184	61.751	70.496	1.00 38.53
ATOM	4731	CB	HIS	A	591	8.094	62.851	72.487	1.00 26.32
ATOM	4732	CG	HIS	A	591	9.219	63.809	72.268	1.00 31.06
ATOM	4733	ND1	HIS	A	591	9.630	64.680	73.255	1.00 32.65
ATOM	4734	CD2	HIS	A	591	9.998	64.032	71.169	1.00 34.91
ATOM	4735	CE1	HIS	A	591	10.635	65.404	72.756	1.00 32.01
ATOM	4736	NE2	HIS	A	591	10.884	65.037	71.508	1.00 33.36
ATOM	4737	N	LYS	A	592	4.978	61.812	72.337	1.00 28.34
ATOM	4738	CA	LYS	A	592	4.254	60.643	71.849	1.00 29.96
ATOM	4739	C	LYS	A	592	3.654	60.692	70.432	1.00 33.41
ATOM	4740	O	LYS	A	592	3.819	59.769	69.592	1.00 29.05
ATOM	4741	CB	LYS	A	592	3.362	59.983	72.888	1.00 32.83
ATOM	4742	CG	LYS	A	592	2.435	60.930	73.615	1.00 31.14
ATOM	4743	CD	LYS	A	592	1.677	60.203	74.704	1.00 38.97
ATOM	4744	CE	LYS	A	592	0.253	60.691	74.890	1.00 25.02
ATOM	4745	NZ	LYS	A	592	-0.157	60.632	76.302	1.00 45.83
ATOM	4746	N	ALA	A	593	2.934	61.782	70.187	1.00 30.97
ATOM	4747	CA	ALA	A	593	2.260	62.026	68.917	1.00 28.47
ATOM	4748	C	ALA	A	593	3.169	61.943	67.703	1.00 32.66
ATOM	4749	O	ALA	A	593	2.775	61.488	66.639	1.00 36.77
ATOM	4750	CB	ALA	A	593	1.571	63.379	68.954	1.00 27.35
ATOM	4751	N	SER	A	594	4.384	62.405	67.869	1.00 27.08
ATOM	4752	CA	SER	A	594	5.345	62.417	66.794	1.00 30.04
ATOM	4753	C	SER	A	594	6.185	61.169	66.760	1.00 36.80
ATOM	4754	O	SER	A	594	6.995	60.991	65.848	1.00 37.94
ATOM	4755	CB	SER	A	594	6.292	63.596	66.977	1.00 37.69
ATOM	4756	OG	SER	A	594	7.199	63.340	68.043	1.00 54.55
ATOM	4757	N	MET	A	595	6.015	60.340	67.776	1.00 33.12
ATOM	4758	CA	MET	A	595	6.794	59.115	67.898	1.00 33.96
ATOM	4759	C	MET	A	595	6.200	57.936	67.125	1.00 40.91
ATOM	4760	O	MET	A	595	5.019	57.927	66.809	1.00 50.82
ATOM	4761	CB	MET	A	595	6.716	58.686	69.382	1.00 34.22
ATOM	4762	CG	MET	A	595	7.621	59.371	70.399	1.00 34.61
ATOM	4763	SD	MET	A	595	7.606	58.440	71.962	1.00 39.24
ATOM	4764	CE	MET	A	595	7.145	59.779	73.084	1.00 36.72
ATOM	4765	N	HIS	A	596	6.987	56.897	66.886	1.00 26.19
ATOM	4766	CA	HIS	A	596	6.496	55.657	66.246	1.00 23.19
ATOM	4767	C	HIS	A	596	5.438	54.964	67.120	1.00 25.21
ATOM	4768	O	HIS	A	596	5.621	54.728	68.311	1.00 22.59
ATOM	4769	CB	HIS	A	596	7.657	54.655	66.077	1.00 24.41

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ATOM   4770  CG  HIS A 596       7.222  53.366  65.493  1.00 30.13
ATOM   4771  ND1 HIS A 596       7.606  52.995  64.214  1.00 32.86
ATOM   4772  CD2 HIS A 596       6.421  52.385  66.005  1.00 30.90
ATOM   4773  CE1 HIS A 596       7.047  51.824  63.974  1.00 30.05
ATOM   4774  NE2 HIS A 596       6.325  51.441  65.031  1.00 30.20
ATOM   4775  N   PRO A 597       4.334  54.587  66.512  1.00 27.08
ATOM   4776  CA  PRO A 597       3.217  53.912  67.173  1.00 26.35
ATOM   4777  C   PRO A 597       3.513  52.851  68.248  1.00 37.51
ATOM   4778  O   PRO A 597       2.979  52.900  69.348  1.00 41.16
ATOM   4779  CB  PRO A 597       2.334  53.307  66.076  1.00 26.17
ATOM   4780  CG  PRO A 597       3.140  53.426  64.792  1.00 34.56
ATOM   4781  CD  PRO A 597       4.285  54.418  65.050  1.00 30.06
ATOM   4782  N   VAL A 598       4.311  51.850  67.939  1.00 33.08
ATOM   4783  CA  VAL A 598       4.585  50.802  68.911  1.00 28.39
ATOM   4784  C   VAL A 598       5.444  51.307  70.029  1.00 29.32
ATOM   4785  O   VAL A 598       5.168  51.096  71.217  1.00 29.13
ATOM   4786  CB  VAL A 598       5.196  49.599  68.210  1.00 27.99
ATOM   4787  CG1 VAL A 598       5.806  48.608  69.187  1.00 26.98
ATOM   4788  CG2 VAL A 598       4.144  48.944  67.296  1.00 26.13
ATOM   4789  N   THR A 599       6.480  52.021  69.635  1.00 26.10
ATOM   4790  CA  THR A 599       7.370  52.573  70.631  1.00 26.95
ATOM   4791  C   THR A 599       6.650  53.404  71.669  1.00 30.81
ATOM   4792  O   THR A 599       6.863  53.327  72.871  1.00 31.33
ATOM   4793  CB  THR A 599       8.413  53.455  69.975  1.00 26.67
ATOM   4794  OG1 THR A 599       9.092  52.725  68.958  1.00 27.92
ATOM   4795  CG2 THR A 599       9.358  53.884  71.092  1.00 20.69
ATOM   4796  N   ALA A 600       5.801  54.218  71.135  1.00 26.41
ATOM   4797  CA  ALA A 600       4.997  55.111  71.878  1.00 26.39
ATOM   4798  C   ALA A 600       4.176  54.339  72.860  1.00 32.00
ATOM   4799  O   ALA A 600       4.162  54.597  74.057  1.00 35.37
ATOM   4800  CB  ALA A 600       4.090  55.774  70.856  1.00 27.56
ATOM   4801  N   MET A 601       3.470  53.380  72.332  1.00 26.26
ATOM   4802  CA  MET A 601       2.627  52.585  73.167  1.00 26.60
ATOM   4803  C   MET A 601       3.439  51.909  74.225  1.00 25.73
ATOM   4804  O   MET A 601       3.099  51.964  75.381  1.00 25.77
ATOM   4805  CB  MET A 601       1.752  51.625  72.353  1.00 30.49
ATOM   4806  CG  MET A 601       1.024  50.594  73.176  1.00 36.00
ATOM   4807  SD  MET A 601       2.043  49.146  73.554  1.00 42.41
ATOM   4808  CE  MET A 601       1.693  48.128  72.111  1.00 37.75
ATOM   4809  N   LEU A 602       4.538  51.310  73.848  1.00 21.64
ATOM   4810  CA  LEU A 602       5.339  50.671  74.873  1.00 22.59
ATOM   4811  C   LEU A 602       6.010  51.650  75.870  1.00 29.61
ATOM   4812  O   LEU A 602       6.137  51.346  77.039  1.00 27.62
ATOM   4813  CB  LEU A 602       6.418  49.760  74.294  1.00 22.14
ATOM   4814  CG  LEU A 602       5.916  48.529  73.575  1.00 25.78
ATOM   4815  CD1 LEU A 602       7.021  48.087  72.609  1.00 26.02
ATOM   4816  CD2 LEU A 602       5.651  47.445  74.613  1.00 21.01
ATOM   4817  N   VAL A 603       6.508  52.805  75.445  1.00 27.15
ATOM   4818  CA  VAL A 603       7.145  53.684  76.413  1.00 26.39
ATOM   4819  C   VAL A 603       6.121  54.157  77.438  1.00 32.60
ATOM   4820  O   VAL A 603       6.436  54.235  78.621  1.00 35.31
ATOM   4821  CB  VAL A 603       7.917  54.832  75.760  1.00 27.78
ATOM   4822  CG1 VAL A 603       8.286  55.887  76.774  1.00 24.54
ATOM   4823  CG2 VAL A 603       9.172  54.286  75.094  1.00 27.29
ATOM   4824  N   GLY A 604       4.878  54.434  76.976  1.00 27.44
ATOM   4825  CA  GLY A 604       3.759  54.856  77.819  1.00 27.58
ATOM   4826  C   GLY A 604       3.418  53.797  78.905  1.00 37.00
ATOM   4827  O   GLY A 604       3.088  54.102  80.072  1.00 36.56
ATOM   4828  N   LYS A 605       3.511  52.522  78.520  1.00 32.54
ATOM   4829  CA  LYS A 605       3.250  51.415  79.459  1.00 32.17
ATOM   4830  C   LYS A 605       4.312  51.405  80.539  1.00 35.15
ATOM   4831  O   LYS A 605       4.040  51.347  81.734  1.00 33.77
ATOM   4832  CB  LYS A 605       3.231  50.034  78.782  1.00 33.59
ATOM   4833  CG  LYS A 605       1.837  49.438  78.576  1.00 42.45
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ATOM   4834  CD  LYS A 605       1.846  48.115  77.815  1.00 60.83
ATOM   4835  CE  LYS A 605       1.223  46.946  78.578  1.00 86.38
ATOM   4836  NZ  LYS A 605       2.188  46.179  79.385  1.00 93.05
ATOM   4837  N   ASP A 606       5.544  51.470  80.056  1.00 32.91
ATOM   4838  CA  ASP A 606       6.715  51.510  80.878  1.00 31.82
ATOM   4839  C   ASP A 606       6.549  52.667  81.833  1.00 36.24
ATOM   4840  O   ASP A 606       6.652  52.503  83.045  1.00 35.19
ATOM   4841  CB  ASP A 606       7.983  51.702  80.027  1.00 32.52
ATOM   4842  CG  ASP A 606       8.302  50.525  79.134  1.00 40.01
ATOM   4843  OD1 ASP A 606       7.934  49.378  79.344  1.00 40.49
ATOM   4844  OD2 ASP A 606       9.038  50.869  78.111  1.00 41.73
ATOM   4845  N   LEU A 607       6.240  53.833  81.266  1.00 34.45
ATOM   4846  CA  LEU A 607       6.152  54.972  82.185  1.00 36.03
ATOM   4847  C   LEU A 607       4.814  55.018  82.968  1.00 42.35
ATOM   4848  O   LEU A 607       4.600  55.872  83.824  1.00 41.57
ATOM   4849  CB  LEU A 607       6.321  56.250  81.364  1.00 36.90
ATOM   4850  CG  LEU A 607       7.779  56.490  80.974  1.00 38.75
ATOM   4851  CD1 LEU A 607       7.954  57.746  80.132  1.00 34.34
ATOM   4852  CD2 LEU A 607       8.695  56.653  82.183  1.00 41.97
ATOM   4853  N   LYS A 608       3.895  54.062  82.586  1.00 45.01
ATOM   4854  CA  LYS A 608       2.576  53.874  83.264  1.00 46.99
ATOM   4855  C   LYS A 608       1.625  55.088  83.181  1.00 51.31
ATOM   4856  O   LYS A 608       0.988  55.467  84.151  1.00 51.35
ATOM   4857  CB  LYS A 608       2.813  53.510  84.750  1.00 50.83
ATOM   4858  CG  LYS A 608       3.331  52.093  84.949  1.00 63.57
ATOM   4859  CD  LYS A 608       4.405  52.019  86.031  1.00 77.03
ATOM   4860  CE  LYS A 608       5.341  50.825  85.858  1.00 96.40
ATOM   4861  NZ  LYS A 608       6.034  50.554  87.117  1.00100.00
ATOM   4862  N   VAL A 609       1.560  55.724  81.991  1.00 50.28
ATOM   4863  CA  VAL A 609       0.688  56.901  81.852  1.00 50.89
ATOM   4864  C   VAL A 609      -0.494  56.660  80.897  1.00 60.23
ATOM   4865  O   VAL A 609      -1.640  56.952  81.194  1.00 63.02
ATOM   4866  CB  VAL A 609       1.533  58.091  81.364  1.00 54.72
ATOM   4867  CG1 VAL A 609       1.996  58.926  82.551  1.00 54.87
ATOM   4868  CG2 VAL A 609       2.744  57.607  80.605  1.00 54.46
ATOM   4869  N   ASP A 610      -0.177  56.152  79.687  1.00 58.84
ATOM   4870  CA  ASP A 610      -1.238  55.949  78.699  1.00 99.84
ATOM   4871  C   ASP A 610      -2.062  54.695  79.001  1.00100.00
ATOM   4872  O   ASP A 610      -3.247  54.615  78.711  1.00 69.75
ATOM   4873  CB  ASP A 610      -0.594  55.818  77.316  1.00100.00
ATOM   4874  CG  ASP A 610      -0.637  57.161  76.610  1.00 92.61
ATOM   4875  OD1 ASP A 610      -1.449  57.999  77.018  1.00 90.49
ATOM   4876  OD2 ASP A 610       0.134  57.355  75.670  1.00 89.29
ATOM   4877 ZN2+ ZN  Z   1      17.003  38.803  64.180  1.00 28.37
ATOM   4878 YB3+ YB  Y   1      43.011  51.068  98.864  1.00 34.70
ATOM   4879 YB3+ YB  Y   2     -13.786  56.771  52.040  0.50 57.25
ATOM   4880 YB3+ YB  Y   3     -10.537  57.860  52.381  0.50 36.57
ATOM   4881  CG  IMD I   1      26.249  42.039  80.754  1.00 28.44
ATOM   4882  ND1 IMD I   1      26.057  42.254  79.400  1.00 28.35
ATOM   4883  CD2 IMD I   1      27.562  41.726  80.902  1.00 17.99
ATOM   4884  CE1 IMD I   1      27.201  42.063  78.760  1.00 29.77
ATOM   4885  NE2 IMD I   1      28.130  41.745  79.647  1.00 35.02
ATOM   4886  CB  ACE C   1      13.616  12.333  68.475  1.00 59.33
ATOM   4887  CG  ACE C   1      12.871  13.331  69.306  1.00 42.98
ATOM   4888  OD1 ACE C   1      12.958  14.536  69.146  1.00 39.66
ATOM   4889  OD2 ACE C   1      12.142  12.759  70.236  1.00 47.21
ATOM   4890  C6  INH V   1       7.422  38.514  70.154  1.00 38.70
ATOM   4891  C5  INH V   1       7.571  39.820  69.689  1.00 37.05
ATOM   4892  C4  INH V   1       7.901  40.062  68.354  1.00 31.41
ATOM   4893  C3  INH V   1       8.091  38.967  67.505  1.00 35.48
ATOM   4894  C2  INH V   1       7.944  37.650  67.949  1.00 31.90
ATOM   4895  C1  INH V   1       7.611  37.434  69.286  1.00 36.93
ATOM   4896  C7  INH V   1       8.071  41.463  67.833  1.00 32.28
ATOM   4897  O1  INH V   1       8.288  41.443  66.485  1.00 37.06
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ATOM	4898	C8	INH	V	1	9.584	41.740	66.129	1.00	32.34
ATOM	4899	C9	INH	V	1	9.825	42.911	65.416	1.00	31.03
ATOM	4900	C10	INH	V	1	11.127	43.216	65.023	1.00	33.64
ATOM	4901	C11	INH	V	1	12.194	42.381	65.339	1.00	31.88
ATOM	4902	C12	INH	V	1	11.928	41.198	66.028	1.00	31.07
ATOM	4903	C13	INH	V	1	10.630	40.858	66.412	1.00	28.70
ATOM	4904	C14	INH	V	1	13.587	42.710	64.882	1.00	32.51
ATOM	4905	C15	INH	V	1	14.260	41.560	64.121	1.00	34.69
ATOM	4906	C16	INH	V	1	15.683	41.849	63.754	1.00	28.88
ATOM	4907	S1	INH	V	1	16.605	40.755	64.790	1.00	29.16
ATOM	4908	N1	INH	V	1	13.497	40.805	63.099	1.00	30.69
ATOM	4909	O	HOH	W	1	44.463	49.888	77.523	1.00	46.91
ATOM	4910	O	HOH	W	2	13.469	27.803	78.018	1.00	20.07
ATOM	4911	O	HOH	W	3	4.225	69.721	58.393	1.00	27.76
ATOM	4912	O	HOH	W	4	15.603	28.826	61.823	1.00	22.81
ATOM	4913	O	HOH	W	5	22.862	26.624	42.874	1.00	53.05
ATOM	4914	O	HOH	W	6	8.423	46.452	57.584	1.00	32.22
ATOM	4915	O	HOH	W	7	17.904	46.550	68.524	1.00	31.91
ATOM	4916	O	HOH	W	8	22.979	45.895	83.716	1.00	39.37
ATOM	4917	O	HOH	W	9	17.707	39.158	55.643	1.00	25.27
ATOM	4918	O	HOH	W	10	12.439	36.303	59.209	1.00	31.46
ATOM	4919	O	HOH	W	11	17.367	62.730	50.320	1.00	37.74
ATOM	4920	O	HOH	W	12	42.823	52.642	90.552	1.00	53.80
ATOM	4921	O	HOH	W	13	34.337	45.508	97.419	1.00	57.99
ATOM	4922	O	HOH	W	14	6.726	27.119	48.459	1.00	62.29
ATOM	4923	O	HOH	W	15	-0.093	30.159	71.746	1.00	29.96
ATOM	4924	O	HOH	W	16	-19.673	44.016	58.682	1.00	58.64
ATOM	4925	O	HOH	W	17	16.563	26.790	80.837	1.00	38.62
ATOM	4926	O	HOH	W	18	10.281	35.677	88.518	1.00	26.01
ATOM	4927	O	HOH	W	19	20.973	35.691	44.774	1.00	49.50
ATOM	4928	O	HOH	W	20	0.996	19.571	53.713	1.00	67.39
ATOM	4929	O	HOH	W	21	20.424	37.014	85.845	1.00	39.54
ATOM	4930	O	HOH	W	22	-2.498	35.905	53.781	1.00	51.70
ATOM	4931	O	HOH	W	23	39.807	49.718	92.595	1.00	37.39
ATOM	4932	O	HOH	W	24	16.431	58.267	93.127	1.00	47.45
ATOM	4933	O	HOH	W	25	6.935	45.104	66.012	1.00	18.12
ATOM	4934	O	HOH	W	26	40.479	54.713	100.253	1.00	28.72
ATOM	4935	O	HOH	W	27	22.369	40.324	67.919	1.00	46.36
ATOM	4936	O	HOH	W	28	37.289	49.457	68.016	1.00	61.37
ATOM	4937	O	HOH	W	29	2.611	35.015	55.709	1.00	24.45
ATOM	4938	O	HOH	W	30	41.088	62.590	98.644	1.00	65.38
ATOM	4939	O	HOH	W	31	17.369	55.024	87.465	1.00	24.22
ATOM	4940	O	HOH	W	32	25.433	20.198	55.692	1.00	44.61
ATOM	4941	O	HOH	W	33	3.890	42.770	66.651	1.00	22.34
ATOM	4942	O	HOH	W	34	3.934	63.391	62.592	1.00	60.69
ATOM	4943	O	HOH	W	35	22.280	41.610	86.289	1.00	74.20
ATOM	4944	O	HOH	W	36	22.631	46.401	90.078	1.00	47.44
ATOM	4945	O	HOH	W	37	33.442	20.227	64.569	1.00	55.41
ATOM	4946	O	HOH	W	38	39.834	28.974	75.602	1.00	41.72
ATOM	4947	O	HOH	W	39	35.232	47.140	54.186	1.00	37.08
ATOM	4948	O	HOH	W	40	36.003	57.784	57.893	1.00	43.05
ATOM	4949	O	HOH	W	41	37.216	27.438	74.564	1.00	50.79
ATOM	4950	O	HOH	W	42	17.770	67.012	77.183	1.00	45.78
ATOM	4951	O	HOH	W	43	5.341	31.286	78.127	1.00	25.34
ATOM	4952	O	HOH	W	44	33.535	32.503	52.063	1.00	56.13
ATOM	4953	O	HOH	W	45	25.477	33.146	44.610	1.00	65.43
ATOM	4954	O	HOH	W	46	16.235	37.438	52.628	1.00	32.10
ATOM	4955	O	HOH	W	47	28.791	14.101	63.316	1.00	46.67
ATOM	4956	O	HOH	W	48	10.230	24.992	86.967	1.00	38.63
ATOM	4957	O	HOH	W	49	30.821	38.856	79.630	1.00	40.44
ATOM	4958	O	HOH	W	50	12.621	37.226	62.944	1.00	26.70
ATOM	4959	O	HOH	W	51	27.987	30.609	66.612	1.00	33.55
ATOM	4960	O	HOH	W	52	34.459	28.696	64.242	1.00	51.01
ATOM	4961	O	HOH	W	53	34.969	62.270	91.179	1.00	68.20

ATOM	4962	O	HOH W	54	33.631	30.717	62.396	1.00	41.64
ATOM	4963	O	HOH W	55	43.987	48.530	91.269	1.00	50.99
ATOM	4964	O	HOH W	56	23.412	28.584	85.186	1.00	69.23
ATOM	4965	O	HOH W	57	39.834	28.057	72.257	1.00	81.00
ATOM	4966	O	HOH W	58	2.892	25.685	69.907	1.00	38.96
ATOM	4967	O	HOH W	59	10.284	47.120	72.671	1.00	40.28
ATOM	4968	O	HOH W	60	32.645	39.037	76.746	1.00	21.71
ATOM	4969	O	HOH W	61	43.535	48.019	95.228	1.00	37.69
ATOM	4970	O	HOH W	62	11.991	51.053	43.479	1.00	41.05
ATOM	4971	O	HOH W	63	18.329	56.527	89.388	1.00	28.51
ATOM	4972	O	HOH W	64	16.555	9.309	68.875	1.00	89.05
ATOM	4973	O	HOH W	65	23.741	44.759	73.150	1.00	38.43
ATOM	4974	O	HOH W	66	19.093	53.805	41.239	1.00	55.25
ATOM	4975	O	HOH W	67	31.750	60.369	56.933	1.00	92.26
ATOM	4976	O	HOH W	68	24.836	68.428	80.926	1.00	59.25
ATOM	4977	O	HOH W	69	-21.014	19.446	48.342	1.00	52.24
ATOM	4978	O	HOH W	70	11.318	68.028	86.566	1.00	77.81
ATOM	4979	O	HOH W	71	5.312	60.076	63.511	1.00	36.83
ATOM	4980	O	HOH W	72	7.689	20.219	84.680	1.00	32.24
ATOM	4981	O	HOH W	73	34.988	44.708	64.746	1.00	40.73
ATOM	4982	O	HOH W	74	10.614	49.644	41.337	1.00	38.90
ATOM	4983	O	HOH W	75	19.349	42.973	64.739	1.00	54.53
ATOM	4984	O	HOH W	76	35.916	30.862	80.753	1.00	55.38
ATOM	4985	O	HOH W	77	9.666	26.046	46.603	1.00	40.09
ATOM	4986	O	HOH W	78	-10.171	46.751	60.237	1.00	29.78
ATOM	4987	O	HOH W	79	46.751	58.883	86.875	1.00	35.92
ATOM	4988	O	HOH W	80	19.320	32.528	51.000	1.00	33.36
ATOM	4989	O	HOH W	81	28.815	39.568	66.176	1.00	59.19
ATOM	4990	O	HOH W	82	38.207	35.773	73.585	1.00	17.81
ATOM	4991	O	HOH W	83	23.802	33.925	75.175	1.00	25.19
ATOM	4992	O	HOH W	84	42.241	51.290	99.896	1.00	15.88
ATOM	4993	O	HOH W	85	3.751	36.678	58.842	1.00	24.97
ATOM	4994	O	HOH W	86	-7.009	40.341	62.580	1.00	25.39
ATOM	4995	O	HOH W	87	11.735	58.910	68.155	1.00	39.70
ATOM	4996	O	HOH W	88	13.986	52.835	42.224	1.00	50.91
ATOM	4997	O	HOH W	89	1.452	46.541	69.459	1.00	35.03
ATOM	4998	O	HOH W	90	-1.938	55.310	56.971	1.00	28.10
ATOM	4999	O	HOH W	91	13.801	66.947	52.600	1.00	38.65
ATOM	5000	O	HOH W	92	21.594	47.218	79.203	1.00	30.31
ATOM	5001	O	HOH W	93	10.639	58.632	90.827	1.00	43.78
ATOM	5002	O	HOH W	94	33.335	53.550	68.086	1.00	37.04
ATOM	5003	O	HOH W	95	-1.984	28.738	60.212	1.00	31.56
ATOM	5004	O	HOH W	96	-4.958	51.055	59.250	1.00	34.00
ATOM	5005	O	HOH W	97	17.610	39.701	51.503	1.00	28.27
ATOM	5006	O	HOH W	98	10.686	54.166	67.565	1.00	37.68
ATOM	5007	O	HOH W	99	20.567	43.859	78.621	1.00	41.57
ATOM	5008	O	HOH W	100	7.013	22.332	69.109	1.00	28.72
ATOM	5009	O	HOH W	101	10.097	53.225	78.477	1.00	35.68
ATOM	5010	O	HOH W	102	10.849	31.404	53.014	1.00	32.22
ATOM	5011	O	HOH W	103	42.381	59.035	94.728	1.00	36.00
ATOM	5012	O	HOH W	104	17.234	41.111	54.082	1.00	33.65
ATOM	5013	O	HOH W	105	26.902	62.025	81.989	1.00	34.70
ATOM	5014	O	HOH W	106	-14.313	49.559	56.204	1.00	54.36
ATOM	5015	O	HOH W	107	41.646	57.501	101.015	1.00	68.12
ATOM	5016	O	HOH W	108	26.759	43.000	47.219	1.00	32.69
ATOM	5017	O	HOH W	109	16.624	48.119	46.545	1.00	38.64
ATOM	5018	O	HOH W	110	26.159	32.793	75.230	1.00	24.77
ATOM	5019	O	HOH W	111	2.101	33.468	67.006	1.00	31.50
ATOM	5020	O	HOH W	112	38.114	36.374	87.451	1.00	44.06
ATOM	5021	O	HOH W	113	13.211	29.810	61.356	1.00	33.81
ATOM	5022	O	HOH W	114	-3.064	37.863	40.673	1.00	37.92
ATOM	5023	O	HOH W	115	15.007	47.948	69.488	1.00	28.23
ATOM	5024	O	HOH W	116	27.101	66.633	80.518	1.00	41.24
ATOM	5025	O	HOH W	117	11.870	38.304	43.174	1.00	40.85

ATOM	5026	O	HOH W 118	-13.844	25.597	58.258	1.00	53.75
ATOM	5027	O	HOH W 119	2.929	41.135	59.858	1.00	36.49
ATOM	5028	O	HOH W 120	24.890	45.490	82.167	1.00	41.65
ATOM	5029	O	HOH W 121	36.062	59.335	75.090	1.00	38.82
ATOM	5030	O	HOH W 122	-10.715	32.037	61.699	1.00	78.82
ATOM	5031	O	HOH W 123	-2.646	25.492	60.812	1.00	48.40
ATOM	5032	O	HOH W 124	-8.948	46.831	63.556	1.00	48.06
ATOM	5033	O	HOH W 125	-17.843	39.367	36.020	1.00	35.80
ATOM	5034	O	HOH W 126	2.218	57.766	62.253	1.00	44.61
ATOM	5035	O	HOH W 127	10.736	62.766	64.366	1.00	55.84
ATOM	5036	O	HOH W 128	0.884	35.562	63.963	1.00	44.14
ATOM	5037	O	HOH W 129	19.165	59.557	60.644	1.00	47.82
ATOM	5038	O	HOH W 130	1.546	27.875	68.443	1.00	39.69
ATOM	5039	O	HOH W 131	5.497	26.285	76.668	1.00	44.47
ATOM	5040	O	HOH W 132	14.505	36.538	88.996	1.00	40.00
ATOM	5041	O	HOH W 133	8.534	28.713	88.519	1.00	46.55
ATOM	5042	O	HOH W 134	6.125	45.267	77.959	1.00	45.57
ATOM	5043	O	HOH W 135	26.016	18.543	78.878	1.00	51.65
ATOM	5044	O	HOH W 136	33.880	23.025	70.739	1.00	46.95
ATOM	5045	O	HOH W 137	19.230	26.073	49.998	1.00	51.97
ATOM	5046	O	HOH W 138	41.563	41.085	77.326	1.00	43.14
ATOM	5047	O	HOH W 139	39.187	63.067	75.380	1.00	56.52
ATOM	5048	O	HOH W 140	26.878	54.491	67.203	1.00	42.14
ATOM	5049	O	HOH W 141	22.988	62.189	74.174	1.00	48.31
ATOM	5050	O	HOH W 142	25.190	62.803	71.067	1.00	67.16
ATOM	5051	O	HOH W 143	18.598	45.126	81.949	1.00	53.80
ATOM	5052	O	HOH W 144	19.782	53.129	90.556	1.00	48.73
ATOM	5053	O	HOH W 145	21.735	48.367	86.454	1.00	40.39
ATOM	5054	O	HOH W 146	25.707	57.012	93.476	1.00	53.61
ATOM	5055	O	HOH W 147	22.832	62.085	93.149	1.00	46.02
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ATOM	5072	O	HOH W 164	21.477	20.377	79.349	1.00	35.96
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ATOM	5077	O	HOH W 169	6.608	51.527	60.826	1.00	39.48
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ATOM	5081	O	HOH W 173	13.799	66.601	85.597	1.00	34.74
ATOM	5082	O	HOH W 174	16.664	53.670	65.006	1.00	43.69
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ATOM	5086	O	HOH W 178	39.940	60.509	78.535	1.00	46.33
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ATOM	5089	O	HOH W 181	17.912	15.338	81.793	1.00	50.08

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ATOM	5099	O	HOH W 191	33.112	26.203	70.484	1.00	60.03
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ATOM	5114	O	HOH W 206	23.953	47.993	67.580	1.00	40.39
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ATOM	5117	O	HOH W 209	21.019	68.985	84.382	1.00	56.50
ATOM	5118	O	HOH W 210	-7.134	33.015	71.591	1.00	56.31
ATOM	5119	O	HOH W 211	40.843	44.050	89.284	1.00	43.07
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ATOM	5123	O	HOH W 215	-2.433	36.012	80.232	1.00	54.12
ATOM	5124	O	HOH W 216	5.257	25.271	55.914	1.00	53.23
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ATOM	5129	O	HOH W 221	32.979	51.667	96.624	1.00	51.30
ATOM	5130	O	HOH W 222	14.677	45.948	71.756	1.00	52.31
ATOM	5131	O	HOH W 223	33.890	24.505	58.094	1.00	43.65
ATOM	5132	O	HOH W 224	17.853	9.519	65.560	1.00	55.94
ATOM	5133	O	HOH W 225	37.794	31.473	62.305	1.00	50.38
ATOM	5134	O	HOH W 226	29.206	50.335	62.673	1.00	45.43
ATOM	5135	O	HOH W 227	4.932	48.808	63.354	1.00	42.45
ATOM	5136	O	HOH W 228	18.933	59.070	55.899	1.00	50.29
ATOM	5137	O	HOH W 229	13.849	18.833	83.641	1.00	55.89
ATOM	5138	O	HOH W 230	25.919	46.022	68.076	1.00	35.63
ATOM	5139	O	HOH W 231	27.565	65.098	75.153	1.00	73.11
ATOM	5140	O	HOH W 232	27.128	39.012	68.497	1.00	40.77
ATOM	5141	O	HOH W 233	40.706	52.468	74.641	1.00	51.60
ATOM	5142	O	HOH W 234	21.689	65.312	58.080	1.00	66.72
ATOM	5143	O	HOH W 235	9.121	17.615	59.271	1.00	51.98
ATOM	5144	O	HOH W 236	17.931	36.565	88.091	1.00	54.77
ATOM	5145	O	HOH W 237	33.843	36.707	52.576	1.00	61.60
ATOM	5146	O	HOH W 238	-3.693	50.074	63.986	1.00	43.64
ATOM	5147	O	HOH W 239	44.272	44.279	81.461	1.00	69.21
ATOM	5148	O	HOH W 240	2.092	28.868	52.894	1.00	54.01
ATOM	5149	O	HOH W 241	8.309	33.518	71.442	1.00	68.05
ATOM	5150	O	HOH W 242	1.051	31.947	69.204	1.00	52.88
ATOM	5151	O	HOH W 243	44.255	51.162	96.650	1.00	20.00
ATOM	5152	O	HOH W 244	16.173	45.408	46.636	1.00	20.00
ATOM	5153	O	HOH W 245	41.130	50.734	97.991	1.00	20.00

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ATOM   5154  O   HOH W 246      36.912  36.263  75.911  1.00 20.00
ATOM   5155  O   HOH W 247     -17.107  27.146  54.728  1.00 20.00
ATOM   5156  O   HOH W 248      24.078  46.307  79.123  1.00 20.00
ATOM   5157  O   HOH W 249     -12.250  47.964  61.593  1.00 20.00
ATOM   5158  O   HOH W 250      35.804  51.343  51.682  1.00 20.00
ATOM   5159  O   HOH W 251      25.537  59.940  69.750  1.00 20.00
ATOM   5160  O   HOH W 252       0.539  55.427  62.088  1.00 20.00
END
```

CLAIMS

1. An isolated protein comprising at least a subsequence of the amino acid sequence of LTA_4 hydrolase, which exhibits a three-dimensional form essentially as disclosed in Table 9 by the parameters defining atom 1 to atom 4876, said subsequence being capable of participating in the control of the an enzymatic pathway, such as the leukotriene cascade, or a functionally equivalent part, derivative or conformational analogue thereof.

2. A protein according to claim 1, which comprises an enzymatically active site defined in the following table:

	Left wall	Right wall
1		Lys608, Asp606, Lys605, Lys354, Thr355
2	Phe356, Phe362	Gln544, Asp573, Lys572, Arg568
3	Val376	Lys565, Arg540, Leu507
4	Ser380, Ser352, Glu348	Pro569
5	Tyr378, Glu348	Arg563, Glu533, Phe536, Arg537, Tyr267
6	Tyr383, Phe314, Glu318, Glu384, Arg326	
7	Gly268, Gly269, Met270	His295, Asn341, Phe340
8	Ser288, His497	Glu325, Asn291

3. A protein according to claim 2, which is an enzyme having a metallohydrolase activity capable of participating in the regulation of enzyme activities in biochemical pathways, wherein said enzymes have structures similar to the ones defined in claim 2.

4. A protein according to claim 1, which comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; Lys565.

5. A protein according to claim 1, which comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Trp315; Glu318; Val322;

Phe362; Val367; Leu369; Pro374; Asp375; Ile372; Ala377; Pro382; Tyr378; Tyr383; Arg563; Lys565.

6. A compound which is substantially complementary to a protein according to any one of claims 1-5.

7. A compound according to claim 6, which is substantially complementary to an enzymatically active site of said protein and which is capable of specifically inhibiting said enzymatic activity.

8. A compound according to claim 7, which is an inhibitor of a metallohydrolase enzyme.

9. An isolated complex, which is comprised of a protein according to claim 1-5 and a complementary compound according to any one of claims 6-8, wherein the three-dimensional structure of LTA_4 hydrolase is essentially as disclosed in Table 9 by the parameters defining atom 1- atom 4876, or a functionally equivalent part, derivative or conformational analogue of such a complex.

10. A complex according to claim 9, wherein the protein complexed with LTA_4 hydrolase is selected from the group which consists of bestatin, thiolamine or hydroxamic acid, or a functionally equivalent part, derivative or conformational analogue of such a complex.

11. Use of the parameters of a protein according to any one of claims 1-5, a compound according to any one of claims 6-8 or a complex according to claim 9 or 10 in drug design, such as in molecular modeling, direct structure-based design and/or combinatorial chemistry.

12. Use according to claim 11, wherein said parameters are selected from the parameters disclosed in Table 9 defining atom 1- atom 4876.

13. Use according to claim 11 or 12, wherein said drug is for the treatment and/or prevention of disorders involving acute and chronic inflammatory and/or allergic symtoms, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis, chronic obstructive pulmonary disease (COPD), and acquired immune deficiency syndrome (AIDS).

14. Use according to claim 11 or 12, wherein said drug is for the treatment and/or prevention of proliferative disorders, such as neoplasias and/or cancer.

15. Use according to claim 11 or 12, wherein said drug is for the treatment and/or prevention of disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax.

16. A method for screening LTA_4 hydrolase analogues that mimic at least a part of the three dimensional structure of the LTA_4 hydrolase molecule as defined by the parameters shown in Table 9 for atom 1 to atom 4876, which comprises the steps of

(a) producing a multiplicity of analogue structures of LTA_4 hydrolase and

(b) selecting an analogue structure, wherein the three-dimensional configuration and spatial arrangement of one or more enzymatically active sites and/or binding sites of said LTA_4 hydrolase remain substantially preserved.

17. A method according to claim 16, wherein an analogue exhibiting an enzymatic activity, such as an epoxide hydrolase and/or aminopeptidase activity, is selected.

18. A method according to claim 16 or 17, wherein an enzymatic inhibitor complementary to the amino acids defined in any one of claims 3, 4 or 5 is screened for.

19. An analogue obtainable by the method according to any one of claims 16-18.

20. An analogue according to claim 19, which exhibits an increased catalytic activity when compared to the naturally occurring form of LTA_4 hydrolase, such as defined in Table 9 by parameters of atom 1 to atom 4876.

21. A method for screening LTA_4 hydrolase binding compounds complementary to a region of LTA_4 hydrolase, preferably an enzymatically active site thereof, which comprises the steps of

(a) producing a multiplicity of possible complementary structures and

(b) selecting a structure, wherein the three-dimensional configuration and spatial arrangement of regions involved in binding to LTA_4 hydrolase remain substantially preserved, which selection is based on the three-dimensional structure of LTA_4 hydrolase, and/or LTA_4 hydrolase complexed to an inhibitor thereof, in a form adopted thereof in nature, such as defined in Table 9.

22. A method according to claim 21, wherein a general metallohydrolase inhibitor is selected, which is capable of inhibiting an enzyme belonging to the M1 family.

23. A method according to claim 21, wherein an inhibitor of the epoxide hydrolase activity and/or aminopeptidase activity of LTA_4 hydrolase or of LTC_4 synthases is selected.

24. A method according to claim 21, wherein a compound capable of antagonizing LTB_4 receptor binding of a cell is selected.

25. A compound obtainable by the method according to any one of claims 21-24.

26. A method of engineering a protein, which method comprises the steps of

-identification of a suitable set of mutations based on the structure of LTA_4 hydrolase;

-generation of a library of genes which contains the suitable sequence variations;

-selection of clones encoding the LTA_4 hydrolase analogues with a desired activity function;

wherein said desired activity is the capability of efficiently producing an organic compound of interest.

27. A method according to claim 26, wherein the specified property is the suicidal mode of action of LTA_4 hydrolase.

28. A process for the purification of a protein according to any one of claims 1-3 or obtained according to claim 26 or 27, which purification includes hydroxyapatite-based chromatography and a subsequent anion exchange chromatography.

29. A process for the crystallisation of an LTA_4 hydrolase, an analogue or a derivative thereof, wherein said crystallisation is performed with the addition of a ytterbium salt as an additive, such as an ytterbium chloride.

30. A protein obtained by the method according to any one of claims 27-29.

31. A protein according to claim 30, which is present in an essentially pure form.

32. An isolated nucleic acid encoding a protein according to claim 30 or 31.

33. A nucleic acid capable of specifically hybridising to a the nucleic acid according to claim 32.

34. Use of a protein, which is a genetically modified LTA_4 hydrolase, according to claim 30 or 31 in the preparation of LTB_4 or other metabolites in the leukotriene cascade.

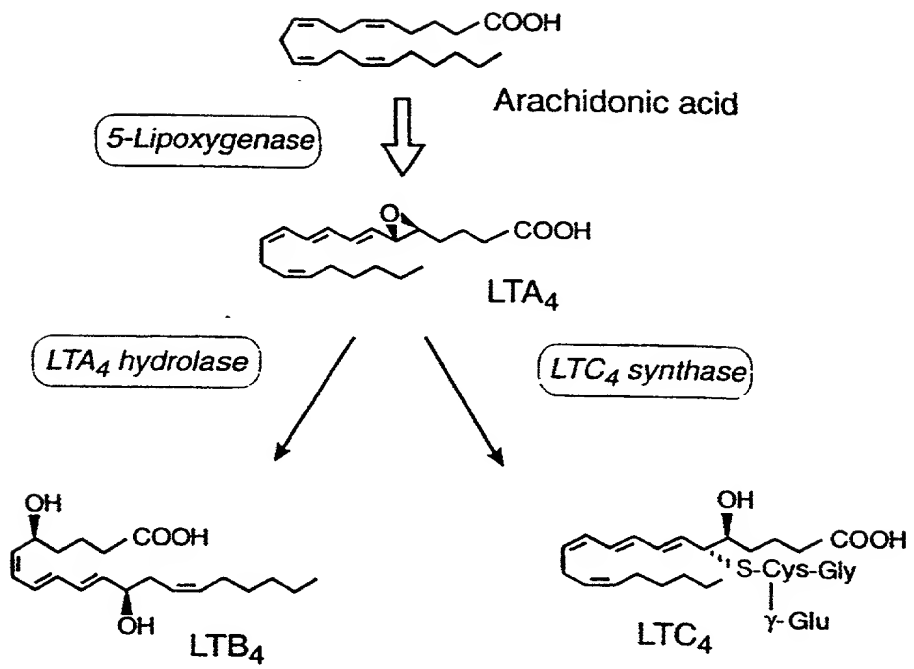
35. A protein according to any one of claims 6-8, 25, 30 or 31 for use as a medicament.

36. Use of a protein according to any one of claims 6-8, 25, 30 or 31 in the manufacture of a medicament for the treatment and/or prevention of acute and chronic inflammatory and/or allergic disorders, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis and chronic obstructive pulmonary disease (COPD); neoplasias and/or cancer; or disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax.

37. Use of a protein according to any one of claims 6-8, 25, 30 or 31, in the manufacture of a medicament for the treatment and/or prevention of an anti-inflammatory and/or anti-allergenic disorder, such as bronchial asthma, allergic rhinitis, conjunctivitis etc.

38. Use of a protein according to any one of claims 6-8, 25, 30 or 31 in the manufacture of a medicament for the treatment and/or prevention of infection caused be human immunodeficiency virus (HIV).

Figure 1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LTA4
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γ-Glu
LTC4

Figure 2

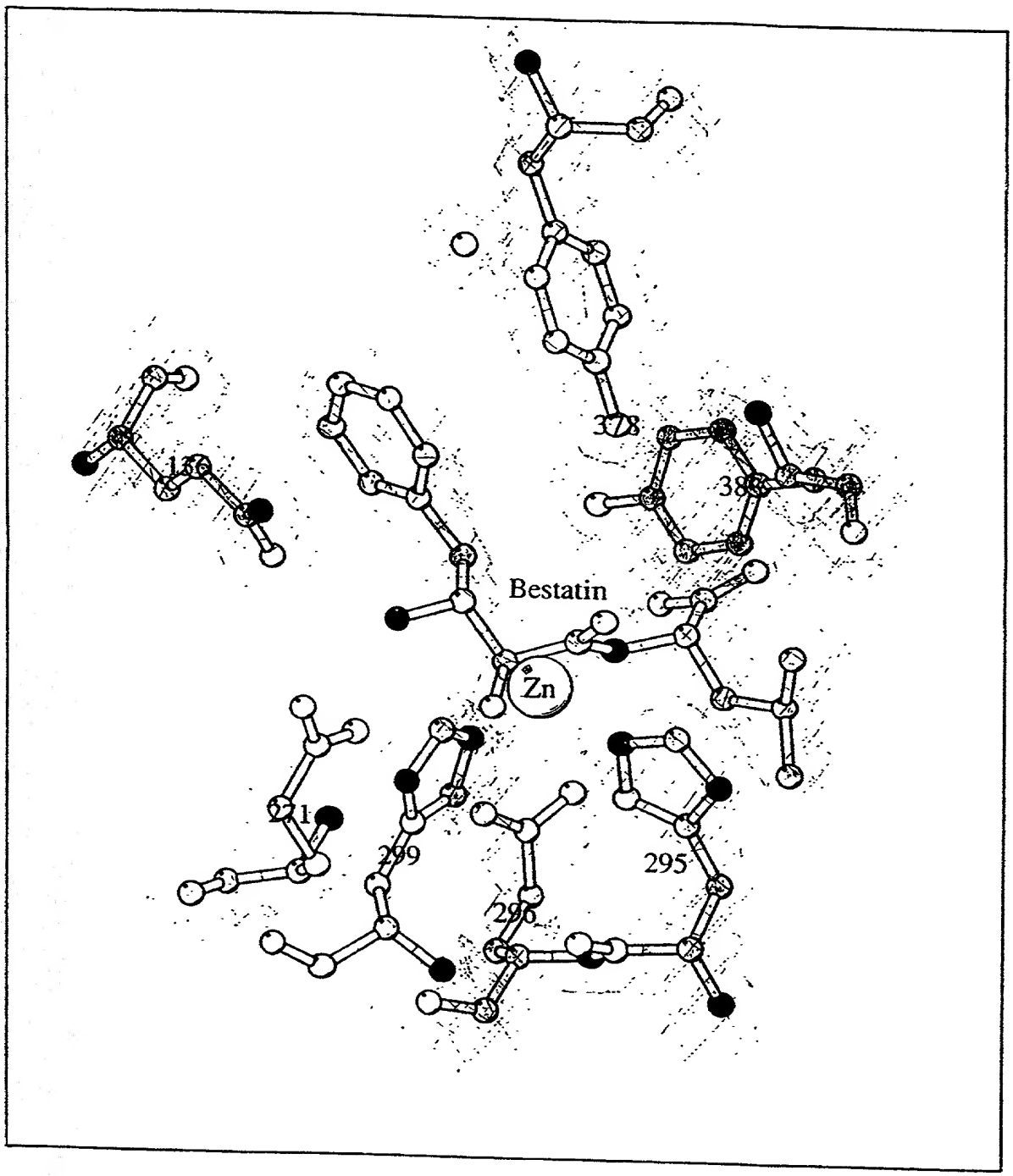

Figure 3

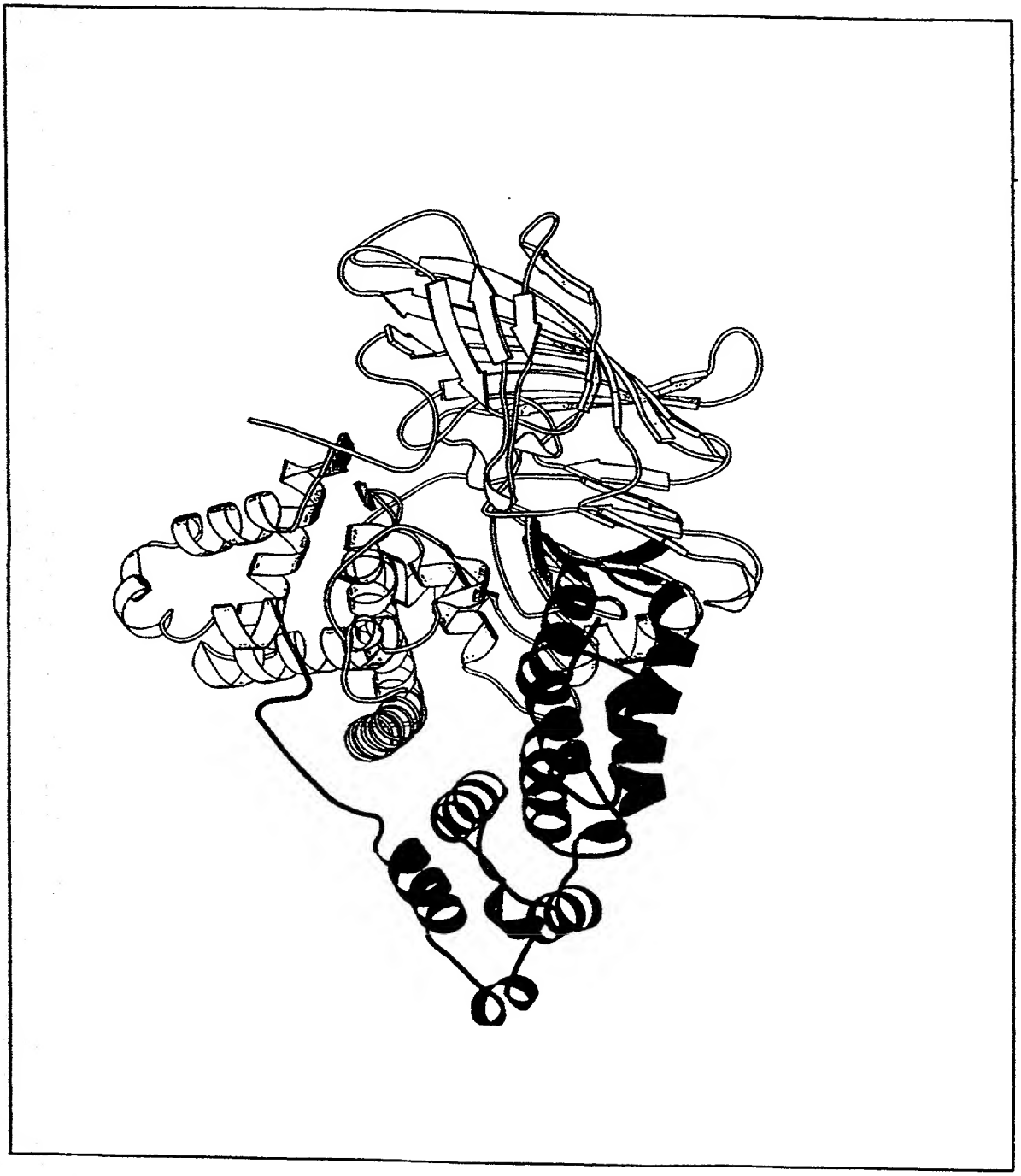

Figure 4a

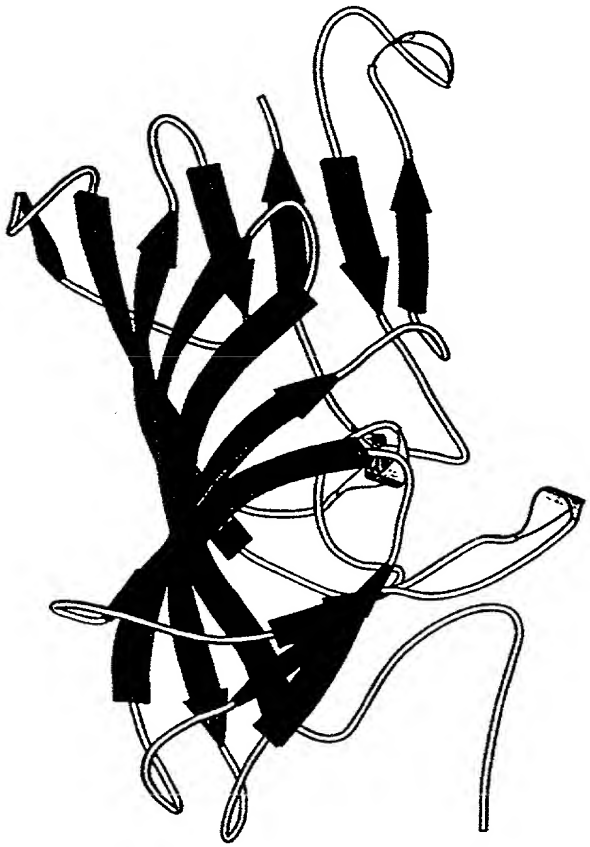

Figure 4b

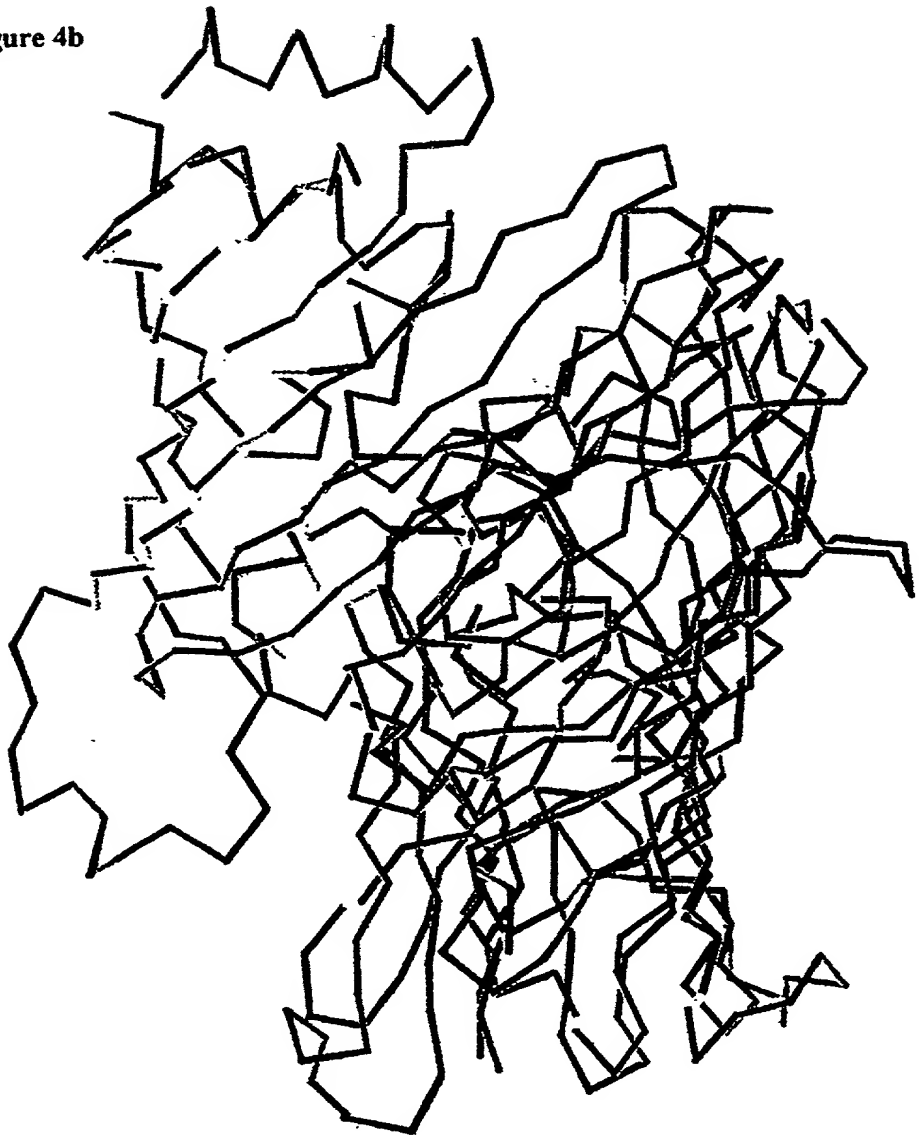

Figure 5a

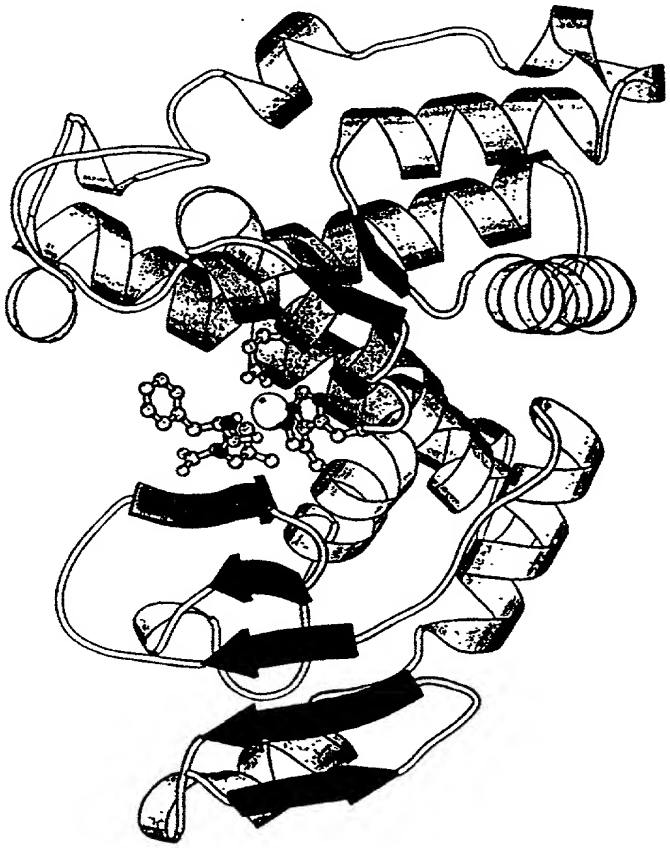

Figure 5b

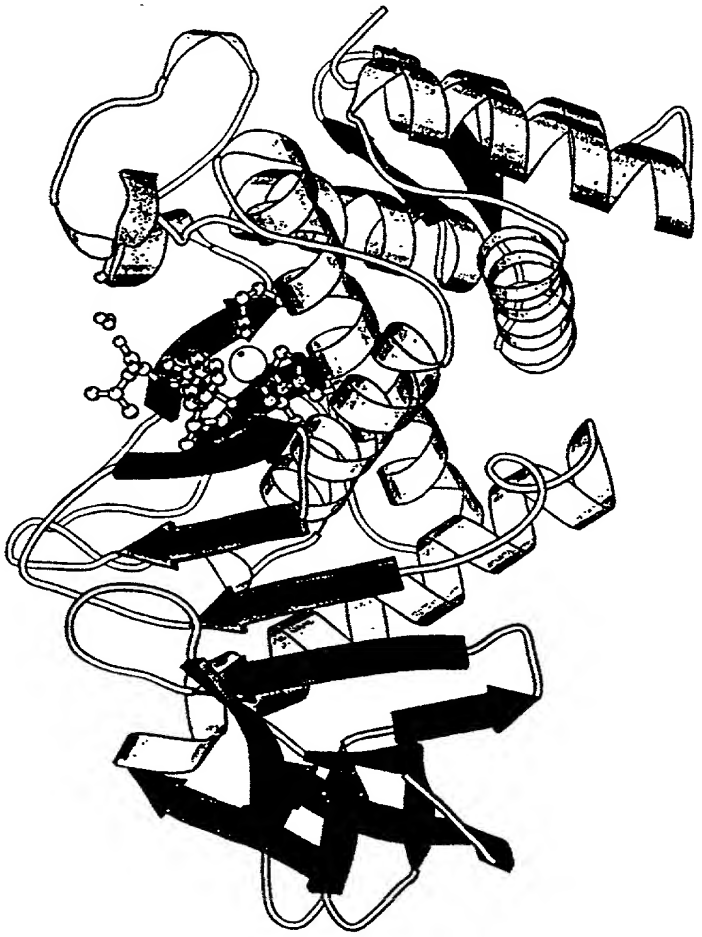

Figure 6

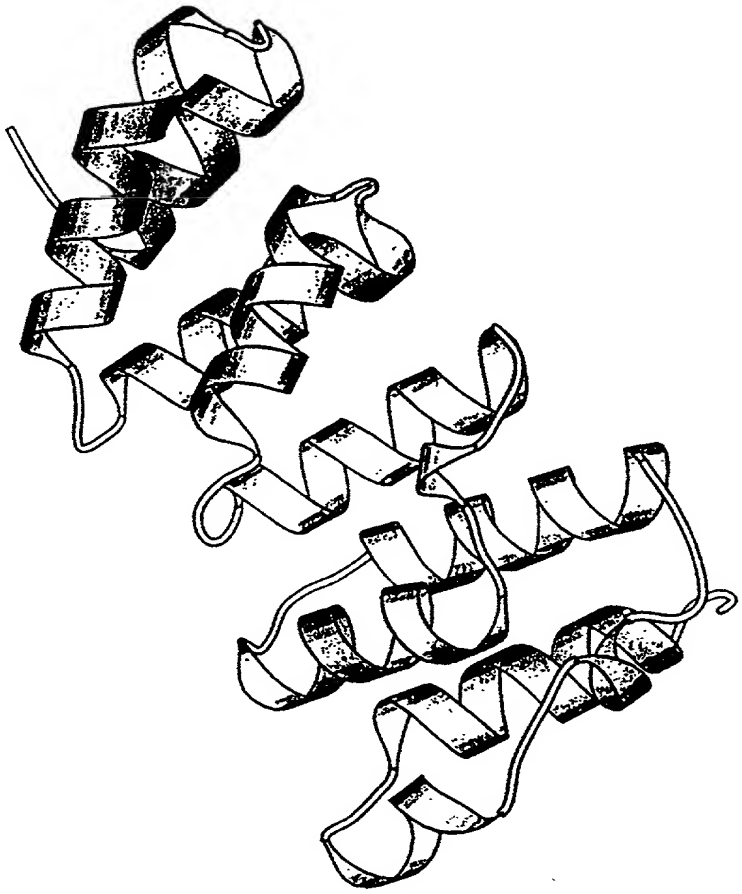

Figure 7

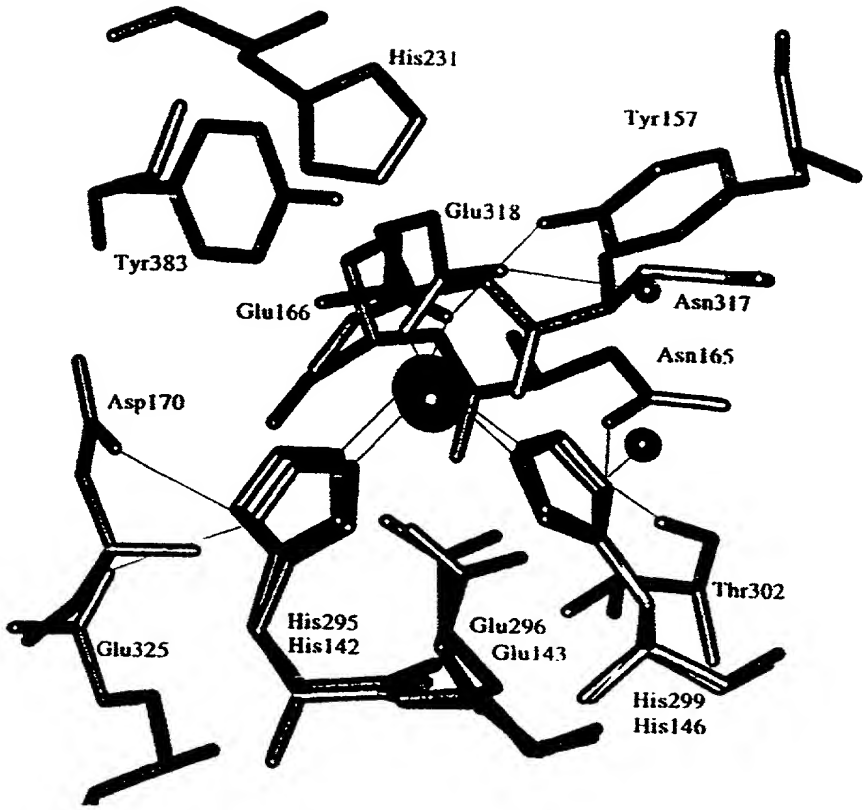
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Figure 8a

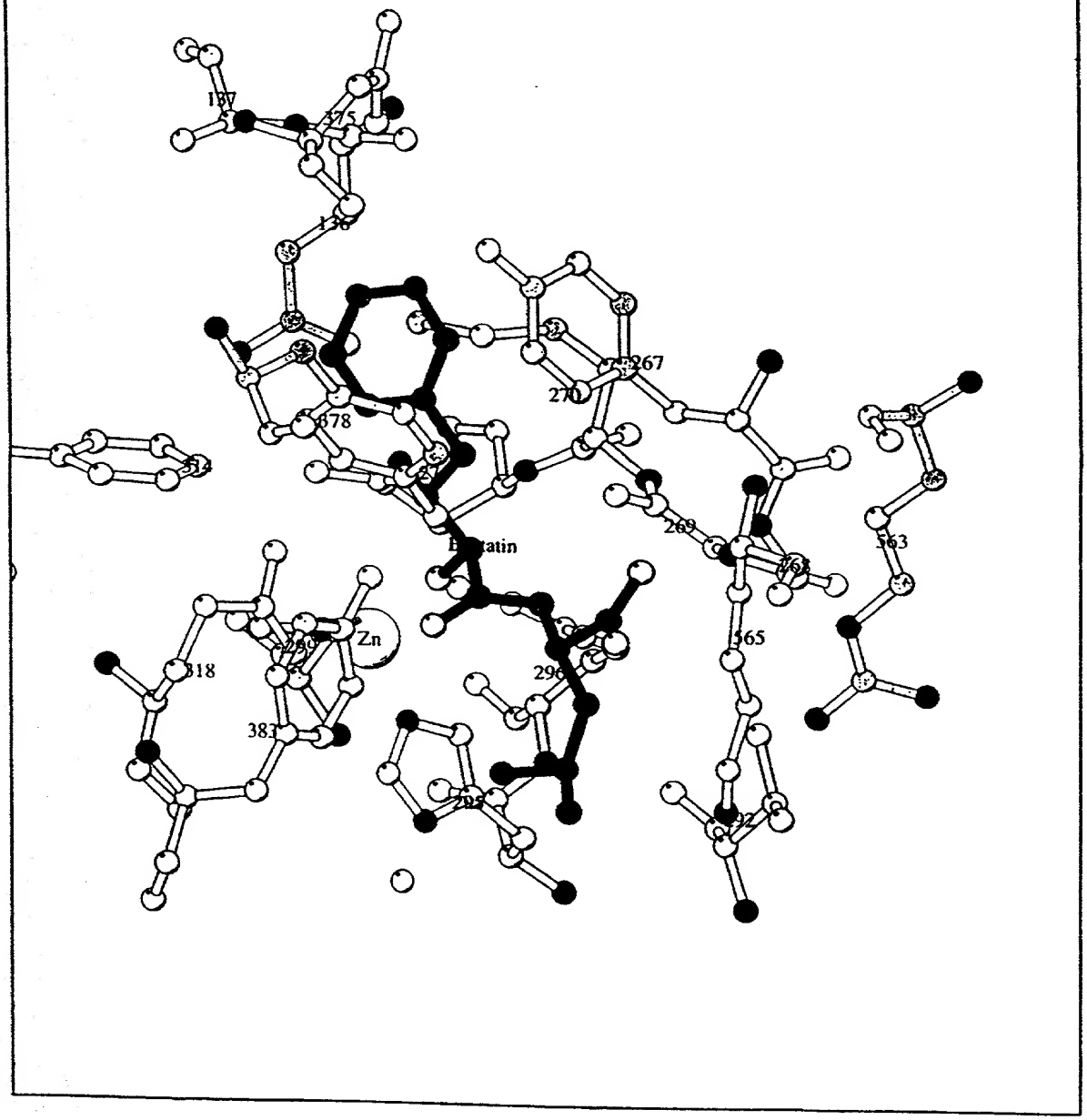
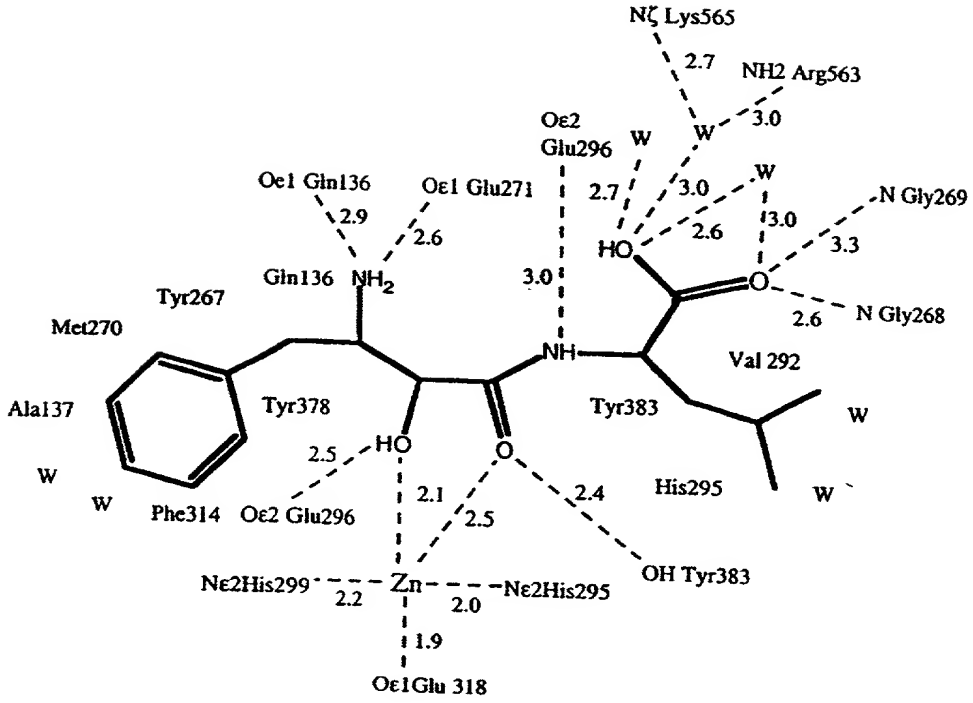


Figure 8b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HO
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O
Tyr267
2.6
N Gly268
Met270
NH
Val 292
Ala137
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Tyr383
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O
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W
His295
W
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2.5
2.4
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Zn
2.0
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OH Tyr383
1.9
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Figure 9a

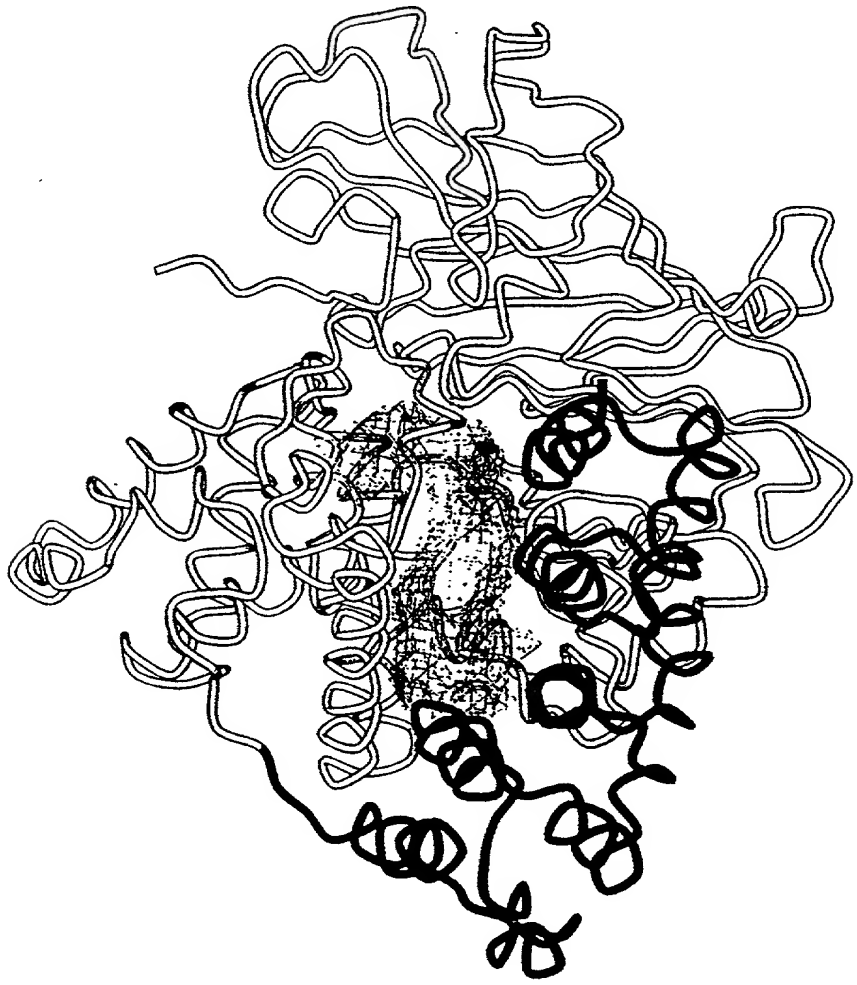

Figure 9b

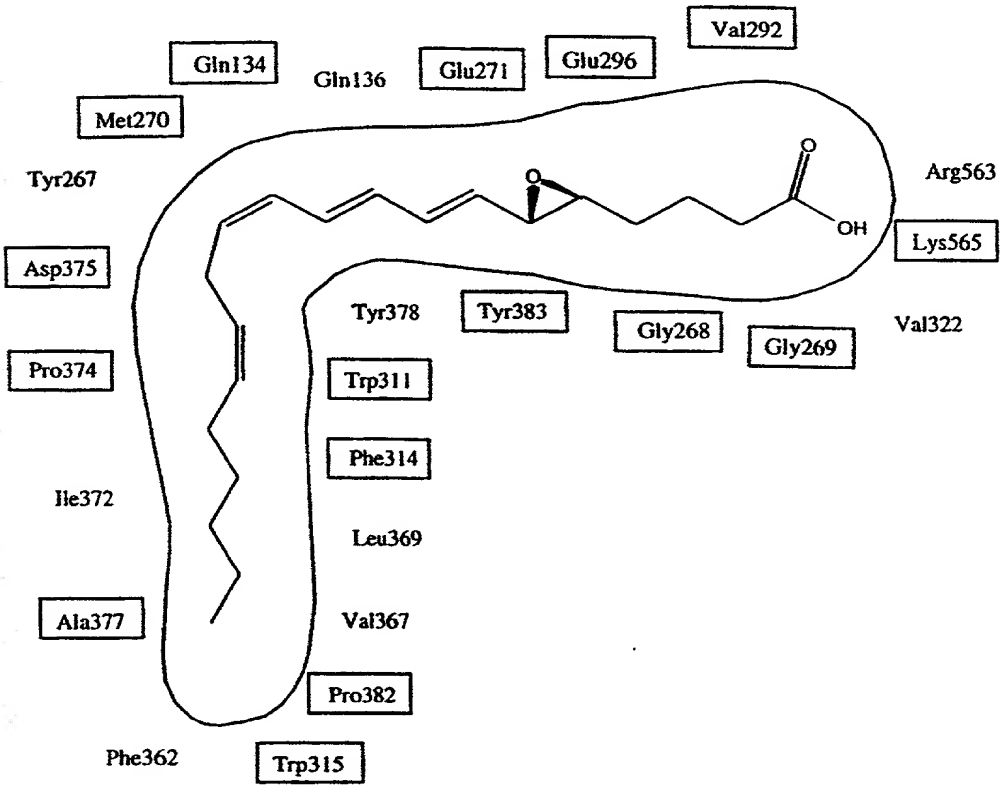
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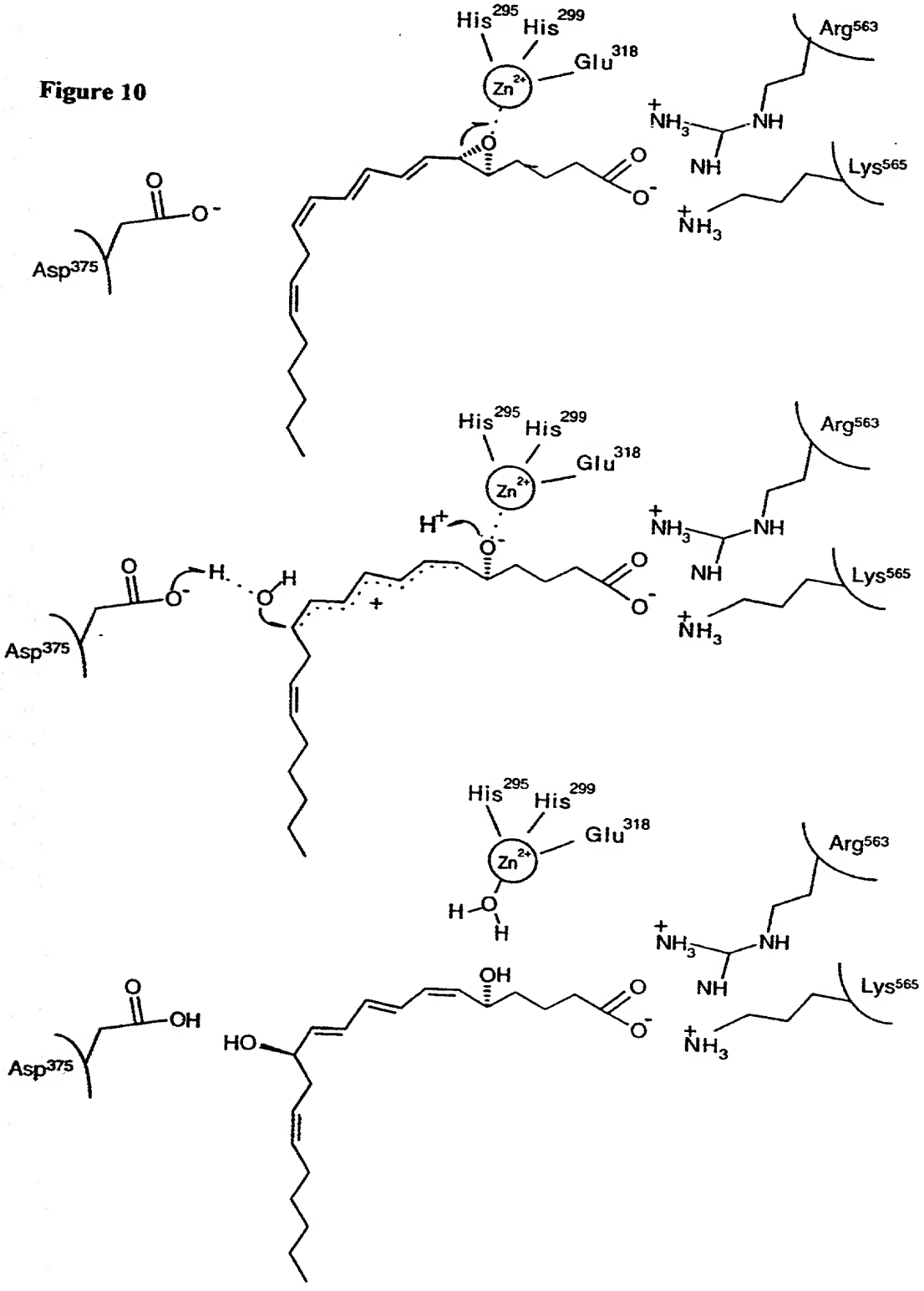
Figure 10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OH
HO

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

(Check one):

- ☒ Declaration Submitted with Initial Filing
- ☐ Declaration Submitted after Initial Filing

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

DRUG DESIGN BASED ON THE STRUCTURE OF LTA_4 HYDROLASE

the specification of which (check one):

☐ is attached hereto.

OR

☒ was filed on **28 February 2000** as PCT International Application Number **PCT/SE00/00384**

- ☐ and was amended by PCT Article 19 Amendment on _____ (if applicable),
- ☐ and was amended by PCT Article 34 Amendment on _____ (if applicable).

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I hereby state that I have reviewed and understood the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

PRIORITY CLAIM

(Check one):

☐ no such applications have been filed.

☒ such applications have been filed as follows

1) FOREIGN PRIORITY CLAIM: I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate or §365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or any PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application Number(s)	Country	Foreign Filing Date (mm,dd,yyyy)	Priority Not Claimed	Certified Copy Attached Yes	Certified Copy Attached No
9900722-1	**SE**	**26 February 1999 (26.02.99)**	☐	☐	☒
			☐	☐	☐

☐ Additional foreign application numbers are listed on a supplemental priority sheet attached hereto.

2) PROVISIONAL PRIORITY CLAIM: I hereby claim the benefit under Title 35, United States Code §119(e) of any United States provisional application(s) listed below.

Provisional Application Number(s)	Filing Date (mm/dd/yyyy)
60/122,110	**26 February 1999 (26.02.99)**

☐ Additional provisional application numbers are listed on a supplemental priority sheet attached hereto.

3) U.S./PCT PRIORITY CLAIM: I hereby claim the benefit under Title 35, United States Code, §120 of any United States application or §365(c) of any PCT international application designating the United States of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose information which is known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

U.S. Parent Application Number	PCT Parent Number	Parent Filing Date (mm/dd/yyyy)	Parent Patent Number *(if applicable)*

☐ Additional U.S. or PCT international application numbers are listed on a supplemental priority sheet attached hereto.

POWER OF ATTORNEY:

As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

James E. Cockfield	Reg. No. 19,162	Megan E. Williams	Reg. No. 43,270
Thomas V. Smurzynski	Reg. No. 24,798	Jeremiah Lynch	Reg. No. 17,425
Ralph A. Loren	Reg. No. 29,325	David J. Rikkers	Reg. No. 43,882
Giulio A. DeConti, Jr.	Reg. No. 31,503	Maria C. Laccotripe	Limited Recognition Under 37 C.F.R. § 10.9(b)
Ann Lamport Hammitte	Reg. No. 34,858		
Elizabeth A. Hanley	Reg. No. 33,505	Debra J. Milasincic	Reg. No. 46,931
Amy E. Mandragouras	Reg. No. 36,207	David R. Burns	Reg. No. 46,590
Anthony A. Laurentano	Reg. No. 38,220	Sean D. Detweiler	Reg. No. 42,482
Kevin J. Canning	Reg. No. 35,470	Peter S. Stecher	Reg. No. 47,259
Jane E. Remillard	Reg. No. 38,872	Cynthia L. Kanik	Reg. No. 37,320
Peter C. Lauro	Reg. No. 32,360	Theodore R. West	Reg. No. 47,202
DeAnn F. Smith	Reg. No. 36,683	Shayne Y. Huff	Reg. No. 44,784
Jeanne M. DiGiorgio	Reg. No. 41,710		

Send Correspondence to:

Elizabeth A. Hanley, Esq. Lahive & Cockfield, LLP, 28 State Street, Boston, Massachusetts 02109, United States of America

Direct Telephone Calls to: (name and telephone number)

Elizabeth A. Hanley, Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of sole or first inventor **HAEGGSTRÖM, Jesper Z.**
Inventor's signature: Jesper Z Haeggström — Date: 2001-11-05
Residence **Valhallavägen 145, SE-115 31 Stockholm, SWEDEN** SE W
Citizenship **SE**
Post Office Address (if different)

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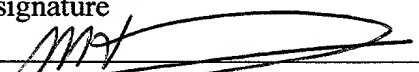
Inventor's signature  Date 2001-11-05
Residence **Gruvbacken 2, SE-116 34 Stockholm, SWEDEN** SE
Citizenship **SE**
Post Office Address (if different)

Full name of third inventor **THUNISSEN, Marjolein**
Inventor's signature  Date 2001-11-05
Residence **Svinningevägen 26, SE-184 92 Åkersberga, SWEDEN** SE
Citizenship **NL**
Post Office Address (if different)

SEQUENCE LISTING

<110> Haeggström et al., Jesper

<120> DRUG DESIGN BASED ON THE STRUCTURE OF LTA_4 HYDROLASE

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Lys Asn Gln Glu Ile Val Ile Glu Ile Ser Phe Glu Thr Ser Pro Lys
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Ile Gln Lys Val Pro Ile Pro Cys Tyr Leu Ile Ala Leu Val Val Gly
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Lys Glu Gln Val Glu Lys Ser Ala Tyr Glu Phe Ser Glu Thr Glu Ser
225 230 235 240

Met Leu Lys Ile Ala Glu Asp Leu Gly Gly Pro Tyr Val Trp Gly Gln
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Tyr Asp Leu Leu Val Leu Pro Pro Ser Phe Pro Tyr Gly Gly Met Glu
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His Thr Val Tyr Leu Glu Arg His Ile Cys Gly Arg Leu Phe Gly Glu
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Lys Phe Arg His Phe Asn Ala Leu Gly Gly Trp Gly Glu Leu Gln Asn
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Pro Glu Ile Phe Leu Gly Phe Leu Lys Ala Tyr Val Glu Lys Phe Ser
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Tyr Lys Ser Ile Thr Thr Asp Asp Trp Lys Asp Phe Leu Tyr Ser Tyr
420 425 430

Phe Lys Asp Lys Val Asp Val Leu Asn Gln Val Asp Trp Asn Ala Trp
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Leu Tyr Ser Pro Gly Leu Pro Pro Ile Lys Pro Asn Tyr Asp Met Thr
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#3

SEQUENCE LISTING

<110> Jesper Z. HAEGGSTRÖM et al.

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